

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:15:53 ; Search time 15 Seconds
(without alignments)
64.090 Million cell updates/sec

Title: US-09-540-816-1
Perfect score: 52
Sequence: 1 EDGIKRIQDD 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	52	100.0	359	2 JCI104	angiotensin II rec
2	52	100.0	359	2 S44425	angiotensin II rec
3	52	100.0	359	2 JCI194	angiotensin II rec
4	52	100.0	359	2 A48857	angiotensin II rec
5	52	100.0	359	2 A42656	angiotensin II rec
6	52	100.0	359	2 J01516	angiotensin II rec
7	52	100.0	359	2 S15403	angiotensin II rec
8	52	100.0	359	2 I39418	angiotensin II rec
9	52	100.0	359	2 JH0621	angiotensin II rec
10	52	100.0	359	2 JCI2134	angiotensin II rec
11	42	80.8	326	2 I40790	angiotensin II rec
12	40	76.9	244	2 G84970	3-oxoacyl-[acyl-ca
13	39	75.0	122	2 T48951	hypothetical prote
14	38	72.1	387	2 G88124	protein ntr-16 [im
15	38	73.1	388	2 T43335	nuclear receptor N
16	37	71.2	538	2 D97369	transcription term
17	37	71.2	538	2 AD2587	N-utilization subs
18	36	69.2	130	2 T15648	hypothetical prote
19	36	69.2	254	2 A64437	hypothetical prote
20	36	69.2	317	2 A59292	probable type II m
21	36	69.2	341	2 AC1528	alpha-1,6-mannas
22	36	69.2	342	2 A11170	alpha-1,6-mannas
23	36	69.2	384	2 T11580	probable 12-oxophy
24	36	69.2	443	2 E82046	protease HslVU
25	36	69.2	464	2 G71082	probable mannose-1
26	36	69.2	465	2 G75104	mannose-6-phosphat
27	36	69.2	595	2 A35847	Fos-related antiage
28	36	69.2	615	2 T29550	hypothetical prote
29	36	69.2	1081	2 T00330	hypothetical prote

30	35	67.3	174	2 C69539	conserved hypothet
31	35	67.3	288	2 B70715	hypothetical prote
32	35	67.3	342	2 T35500	6-phosphofructokin
33	35	67.3	455	2 S31806	emp3 protein - mal
34	35	67.3	681	2 T15590	hypothetical prote
35	35	67.3	782	2 G96698	hypothetical prote
36	35	67.3	829	2 S58888	Ins p4-binding pro
37	35	67.3	829	2 S71847	Ins p4-binding pro
38	35	67.3	1400	2 T22644	hypothetical prote
39	35	67.3	1548	2 T25808	hypothetical prote
40	35	67.3	2441	2 D71623	erythrocyte membra
41	34	65.4	62	2 E84420	probable ubiquinol
42	34	65.4	126	2 S29303	hypothetical prote
43	34	65.4	184	2 A70115	ribosome releasing
44	34	65.4	207	2 F70135	flagellar protein
45	34	65.4	224	2 T39771	hypothetical prote

ALIGNMENTS

RESULT 1
JCI104
angiotensin II receptor type 1 - human
N:Alternate names: angiotensin II receptor 1A
C:Species: Homo sapiens (man)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jul-2000
C:Accession: JCI104; J01402; JH0574; JH0267; A44014; S18983
R:Maizy, C.A.; Hwang, O.; Egloff, A.M.; Wu, L.H.; Chung, F.Z.
Biochem. Biophys. Res. Commun. 186, 277-284, 1992
A:Title: Cloning, expression, and characterization of a gene encoding the human angio
A:Reference number: JCI104; MUID:92337608; PMID:1376723
A:Accession: JCI104
A:Molecule type: DNA
A:Residues: 1-359 <MAU>
R:Furuta, H.; Guo, D.F.; Inagami, T.
Biochem. Biophys. Res. Commun. 183, 8-13, 1992
A:Title: Molecular cloning and sequencing of the gene encoding human angiotensin II t
A:Reference number: J01402; MUID:92181475; PMID:1543512
A:Accession: J01402
A:Molecule type: DNA
A:Residues: 1-359 <FUR>
A:Cross-references: EMBL:Z11162; NID:g28709; PID:g28710
A:Experimental source: Lymphocyte
R:Berghma, D.J.; Ellis, C.; Kumar, C.; Nuthulaganti, P.; Kersten, H.; Elshourbagy, N.
Biochem. Biophys. Res. Commun. 183, 989-995, 1992
A:Title: Cloning and characterization of a human angiotensin II type 1 receptor.
A:Reference number: JH0574; MUID:92231907; PMID:1567413
A:Accession: JH0574
A:Molecule type: mRNA
A:Residues: 1-359 <BER>
A:Cross-references: GB:M07290; NID:g178682; PID:AAA35535.1; PID:g178683
A:Experimental source: Liver
R:Takayanagi, R.; Ohnaka, K.; Sakai, Y.; Nakao, R.; Yanase, T.; Hajl, M.; Inagami, T.
Biochem. Biophys. Res. Commun. 183, 910-916, 1992
A:Title: Molecular cloning, sequence analysis and expression of a cDNA encoding human
A:Reference number: JH0267; MUID:92198490; PMID:1550596
A:Accession: JH0267
A:Molecule type: mRNA
A:Residues: 1-359 <TAK>
A:Experimental source: Liver
R:Turnow, K.M.; Pascoe, L.; White, P.C.
Mol. Endocrinol. 6, 1113-1118, 1992
A:Title: Genetic analysis of the human type-1 angiotensin II receptor.
A:Reference number: A44014; MUID:92375105; PMID:1508224
A:Accession: A44014
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <CUR>
A:Cross-references: GB:M93394; NID:g178680; PID:g178681
A:Note: sequence extracted from NCBI backbone (NCBIN:111831, NCBIPI:111833)
C:Genetics:
A:Gene: GDB:AGTR1

A:Cross-references: GDB:133359; OMIM:106165
A:Map position: 3q21-3q25
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; transmembrane protein
F:30-53/Domain: transmembrane #status predicted <TM1>
F:65-90/Domain: transmembrane #status predicted <TM2>
F:103-124/Domain: transmembrane #status predicted <TM3>
F:145-167/Domain: transmembrane #status predicted <TM4>
F:194-216/Domain: transmembrane #status predicted <TM5>
F:241-264/Domain: transmembrane #status predicted <TM6>
F:281-305/Domain: transmembrane #status predicted <TM7>
F:4,176,188/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match
Best Local Similarity 100.0%; Score 52; DB 2; Length 359;
Pred. No. 0.062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGKRIQDD 10
|||||
Db 8 EDGKRIQDD 17

RESULT 2
S44425
angiotensin II receptor type 1 - dog
C:Species: Canis lupus familiaris (dog)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C:Accession: S44425
R:Burns, L.; Bradley, J.; Robertson, M.J.; Clark, A.J.L.
FEBS Lett. 343, 146-150, 1994
A:Title: Molecular cloning of the canine angiotensin II receptor. An AT1-like receptor
A:Reference number: S44425; MUID:94222188; PMID:8168620
A:Accession: S44425
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-359 <BUR>
A:Cross-references: PIDN:AAB30674.1; PID:9546569
A:Experimental source: liver
C:Superfamily: vertebrate rhodopsin

Query Match
Best Local Similarity 100.0%; Score 52; DB 2; Length 359;
Pred. No. 0.062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGKRIQDD 10
|||||
Db 8 EDGKRIQDD 17

RESULT 3
JC1194
angiotensin II receptor 1B - mouse
C:Species: Mus musculus (house mouse)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 05-Nov-1999
C:Accession: JC1194; JH0622
R:Yoshida, H.; Kakuchi, J.; Guo, D.F.; Furuta, H.; Iwai, N.; van der Meer-de Jong, R.; I
Biochem. Biophys. Res. Commun. 186, 1042-1049, 1992
A:Title: Analysis of the evolution of angiotensin II type 1 receptor gene in mammals (mo
A:Reference number: JC1193; MUID:92359981; PMID:1497638
A:Accession: JC1194
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-359 <YOS>
R:Sasamura, H.; Hein, L.; Krieger, J.E.; Pratt, R.E.; Kobilka, B.K.; Dzau, V.J.
Biochem. Biophys. Res. Commun. 185, 253-259, 1992
A:Title: Cloning, characterization, and expression of two angiotensin receptor (AT-1) is
A:Accession: JH0622; MUID:92287102; PMID:1599461
A:Molecule type: DNA
A:Residues: 1-6, 'I', '8-165, 'H', '167-172, 'E', '174-204, 'V', '206-231, 'T', '233-238, 'F', '240-359 <S
A:Cross-references: GB:S37491; NID:9245947; PIDN:AAB2220.1; PID:9245948
A:Experimental source: Balb/c
C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p
F:30-53/Domain: transmembrane #status predicted <TM1>
F:65-90/Domain: transmembrane #status predicted <TM2>
F:103-123/Domain: transmembrane #status predicted <TM3>
F:147-166/Domain: transmembrane #status predicted <TM4>
F:195-218/Domain: transmembrane #status predicted <TM5>
F:240-263/Domain: transmembrane #status predicted <TM6>
F:278-300/Domain: transmembrane #status predicted <TM7>
F:4,176,188/Binding site: carboxylate (Asn) (covalent) #status predicted
F:141/Binding site: phosphate (Thr) (covalent) #status predicted
F:331,338,348/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match
Best Local Similarity 100.0%; Score 52; DB 2; Length 359;
Pred. No. 0.062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGKRIQDD 10
|||||
Db 8 EDGKRIQDD 17

RESULT 4
A48857
angiotensin II receptor type 1 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C:Accession: A48857
R:Burns, K.D.; Inagami, T.; Harris, R.C.
Am. J. Physiol. 264, F645-F654, 1993
A:Title: Cloning of a rabbit kidney cortex AT1 angiotensin II receptor that is presen
A:Reference number: A48857; MUID:93236091; PMID:7916579
A:Accession: A48857
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-359 <BUR>
A:Cross-references: GB:S59041; NID:9299614; PIDN:AAB26239.1; PID:9299615
A:Experimental source: proximal tubule cells
A:Note: sequence extracted from NCBI backbone (NCBIN:129600, NCBIPI:129601)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match
Best Local Similarity 100.0%; Score 52; DB 2; Length 359;
Pred. No. 0.062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGKRIQDD 10
|||||
Db 8 EDGKRIQDD 17

RESULT 5
A42656
angiotensin II receptor type 1B (AT3) - rat
N:Alternate names: angiotensin II receptor chain B
C:Species: Rattus norvegicus (Norway rat)
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C:Accession: A42656; S20423
R:Sandberg, K.; Ji, H.; Clark, A.J.; Shapiro, H.; Catt, K.J.
J. Biol. Chem. 267, 9455-9458, 1992
A:Title: Cloning and expression of a novel angiotensin II receptor subtype.
A:Reference number: A42656; MUID:92250585; PMID:1374402
A:Accession: A42656
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <SAN>
A:Cross-references: GB:M90065; NID:9202801; PIDN:AAA40704.1; PID:9202802
A:Experimental source: adrenal cortex
A:Note: sequence extracted from NCBI backbone (NCBIN:100262, NCBIPI:100268)
R:Iwai, N.; Inagami, T.
FEBS Lett. 298, 257-260, 1992
A:Title: Identification of two subtypes in the rat type I angiotensin II receptor.
A:Reference number: S20423; MUID:92183879; PMID:1544458
A:Accession: S20423

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <IYMA>
A:Cross-references: GB:X64052; NID:g57521; PIDN:CAA45410.1; PID:g57522
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 100.0%; Score 52; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EDGIRRIODD 10
Db 8 EDGIRRIODD 17

RESULT 6

J01516
angiotensin II receptor type 1b - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999
C:Accession: J01516; JH0578; PH0850
R:Elton, T.S.; Stephan, C.C.; Taylor, G.R.; Kimball, M.G.; Martin, M.M.; Durand, J.N.; C
Biochem. Biophys. Res. Commun. 184, 1067-1073, 1992
A:Title: Isolation of two distinct type 1 angiotensin II receptor genes.
A:Reference number: J01516; MUID:92246922; PMID:1575725
A:Accession: J01516

A:Molecule type: DNA
A:Residues: 1-359 <ELTY>
A>Note: the authors translated the codon AGC for residue 120 as Thr, GTC for residue 225
R:Kakar, S.S.; Sellers, J.C.; Devor, D.C.; Musgrove, L.C.; Neill, J.D.
Biochem. Biophys. Res. Commun. 183, 1090-1096, 1992

A:Title: Angiotensin II type-1 receptor subtype cDNAs: differential tissue expression at
A:Reference number: JH0578; MUID:92231868; PMID:1567388
A:Accession: JH0578

A:Molecule type: mRNA
A:Residues: 1-74, 'V', '76-119, 'T', '121-224, 'A', '226-359 <RKK>
A:Cross-references: GB:M87003; NID:g202920; PIDN:AAA40739.1; PID:g202921
A:Experimental source: anterior pituitary

R:Ye, M.O.; Healy, D.P.
Biochem. Biophys. Res. Commun. 185, 204-210, 1992
A:Title: Characterization of an angiotensin type-1 receptor partial cDNA from rat kidney
A:Reference number: PH0850; MUID:92287094; PMID:1599457
A:Accession: PH0850

A:Molecule type: mRNA
A:Residues: 84-119, 'T', '121-224, 'A', '226-259 <YEM>
A:Cross-references: GB:S37461; NID:g249938; PIDN:AB22267.1; PID:g249939
A:Experimental source: kidney
C:Genetics:

A:Gene: AT1B
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
F:27-53/Domain: transmembrane #status predicted <TM1>
F:65-90/Domain: transmembrane #status predicted <TM2>
F:103-125/Domain: transmembrane #status predicted <TM3>
F:145-166/Domain: transmembrane #status predicted <TM4>
F:194-216/Domain: transmembrane #status predicted <TM5>
F:240-264/Domain: transmembrane #status predicted <TM6>
F:278-304/Domain: transmembrane #status predicted <TM7>
F:314-333/Domain: transmembrane #status predicted <TM8>
F:333-333/Binding site: carbohydrate (asn) (covalent) #status predicted
F:331,338,348/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 100.0%; Score 52; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EDGIRRIODD 10
Db 8 EDGIRRIODD 17

RESULT 7

S15403
angiotensin II receptor type 1 - bovine
C:Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C:Accession: S15403
R:Sasaki, K.; Yamano, Y.; Bardhan, S.; Iwai, N.; Murray, J.J.; Hasegawa, M.; Matsuda,
Nature 351, 230-233, 1991

A:Title: Cloning and expression of a complementary DNA encoding a bovine adrenal ang1
A:Reference number: S15403; MUID:91251900; PMID:2041569
A:Accession: S15403

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <SAS>
A:Cross-references: GB:X62294; NID:g43; PIDN:CAA4182.1; PID:g44
C:Superfamily: vertebrate rhodopsin

Query Match 100.0%; Score 52; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EDGIRRIODD 10
Db 8 EDGIRRIODD 17

RESULT 8

I39418
angiotensin II receptor type 1b - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 24-Nov-1999
C:Accession: I39418
R:Kuroda, S.

Biochem. Biophys. Res. Commun. 199, 467-474, 1994
A:Title: Novel subtype of human angiotensin II type 1 receptor: cDNA cloning and expr
A:Reference number: I39418; MUID:94183213; PMID:8135787
A:Accession: I39418

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-359 <RES>
A:Cross-references: GB:D13814; NID:g471120; PIDN:BA02968.1; PID:g471121
C:Superfamily: vertebrate rhodopsin

Query Match 100.0%; Score 52; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EDGIRRIODD 10
Db 8 EDGIRRIODD 17

RESULT 9

JH0621
angiotensin II receptor 1A - mouse
C:Species: Mus musculus (house mouse)
C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 24-Nov-1999
C:Accession: JH0621; J01193
R:Sasamura, H.; Hein, L.; Krieger, J.E.; Pratt, R.E.; Koblika, B.K.; Dzau, V.J.

Biochem. Biophys. Res. Commun. 185, 253-259, 1992
A:Title: Cloning, characterization, and expression of two angiotensin receptor (AT-1)
A:Reference number: JH0621; MUID:92287102; PMID:1599461
A:Accession: JH0621

A:Molecule type: DNA
A:Residues: 1-359 <SAS>
A:Cross-references: GB:S37484; NID:g249945; PIDN:AB22269.1; PID:g249946
A:Experimental source: strain Balb/c

R:Yoshida, H.; Kakuchi, J.; Guo, D.F.; Furuta, H.; Iwai, N.; van der Meer-de Jong, R.
Biochem. Biophys. Res. Commun. 186, 1042-1049, 1992
A:Title: Analysis of the evolution of angiotensin II type 1 receptor gene in mammals
A:Reference number: J01193; MUID:9235981; PMID:1497638
A:Accession: J01193

A:Status: nucleic acid sequence not shown
A:Molecule type: DNA

A.Residues: 1-6,'I',8-19,'IS',22-37,'W',39-133,'K',135-359 <YOS>
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
F:37-57/Domain: transmembrane #status predicted <TM1>
F:65-85/Domain: transmembrane #status predicted <TM2>
F:103-123/Domain: transmembrane #status predicted <TM3>
F:145-165/Domain: transmembrane #status predicted <TM4>
F:201-220/Domain: transmembrane #status predicted <TM5>
F:241-261/Domain: transmembrane #status predicted <TM6>
F:286-306/Domain: transmembrane #status predicted <TM7>
F:4176.188/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:331.338/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 100.0%; Score 52; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGKRIQDD 10
Db 8 EDGKRIQDD 17

RESULT 10

JC2134
angiotensin II receptor type 1A - rat
N:Alternate names: AT1a receptor; AT3 receptor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 24-Nov-1999
C:Accession: J02134; S15404; S20424; J01055
R:Conchon, S.; Monnot, C.; Sirriex, M.E.; Bihoreau, C.; Corvol, P.; Clausen, E.
Biochem. Biophys. Res. Commun. 199, 1347-1354, 1994
A:Title: Synthetic cDNA encoding the rat AT1a receptor: a useful tool for structure-func
A:Reference number: JC2134; MUID:94197726; PMID:8147879
A:Accession: JC2134
A:Molecule type: mRNA
A.Residues: 1-359 <CON>
A>Note: the amino acid sequence of this protein is not given
R:Murphy, T.J.; Alexander, R.W.; Griendling, K.K.; Runge, M.S.; Bernstein, K.E.
Nature 351, 233-236, 1991
A:Title: Isolation of a cDNA encoding the vascular type-1 angiotensin II receptor.
A:Reference number: S15404; MUID:91251901; PMID:2041570
A:Accession: S15404
A:Status: preliminary
A:Molecule type: mRNA
A.Residues: 1-359 <MUR>
A:Cross-references: GB:X62295; NID:957773; PIDN:CAA44183.1; PID:957774
R:Iwai, N.; Inagami, T.
FEBS Lett. 298, 257-260, 1992
A:Title: Identification of two subtypes in the rat type I angiotensin II receptor.
A:Reference number: S20423; MUID:92183879; PMID:1544458
A:Accession: S20424
A:Status: preliminary
A:Molecule type: mRNA
A.Residues: 1-359 <IWA>
R:Iwai, N.; Yamano, Y.; Chaki, S.; Konishi, F.; Barchan, S.; Tibbets, C.; Sasaki, K.; H
Biochem. Biophys. Res. Commun. 177, 299-304, 1991
A:Title: Rat angiotensin II receptor: cDNA sequence and regulation of the gene expressio
A:Reference number: J01055; MUID:91254291; PMID:2043116
A:Accession: J01055
A:Molecule type: mRNA
A.Residues: 1-80,'C',82-108,'T',110-359 <IW2>
A:Cross-references: GB:M74054; NID:9202918; PIDN:AAA40738.1; PID:9202919
A:Experimental source: kidney
C:Comment: AT1 receptor consists of two closely related AT1 isoforms of angiotensin II r
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; GTP binding; receptor; transmembra
F:27-86/Domain: transmembrane #status predicted <TM1>
F:103-123/Domain: transmembrane #status predicted <TM3>
F:147-167/Domain: transmembrane #status predicted <TM4>
F:195-218/Domain: transmembrane #status predicted <TM5>
F:240-263/Domain: transmembrane #status predicted <TM6>
F:278-299/Domain: transmembrane #status predicted <TM7>
F:4176.188/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 52; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGKRIQDD 10
Db 8 EDGKRIQDD 17

RESULT 11

I40790
acetoin dehydrogenase (TPP-dependent) (EC 1.-.-.-) alpha chain - Clostridium magnum
C:Species: Clostridium magnum
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 15-Oct-1999
C:Accession: I40790
R:Kruger, N.; Oppermann, F.B.; Lorenz, H.; Steinhüchel, A.
J. Bacteriol. 176, 3614-3630, 1994
A:Title: Biochemical and molecular characterization of the Clostridium magnum acetoin
A:Reference number: I40789; MUID:94266715; PMID:8206840
A:Accession: I40790
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A.Residues: 1-326 <KRU>
A:Cross-references: GB:L31844; NID:9472324; PIDN:AAA21744.1; PID:9472326
C:Genetics:
A:Start codon: TTG
C:Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-
C:Keywords: oxidoreductase

Query Match 80.8%; Score 42; DB 2; Length 326;
Best Local Similarity 70.0%; Pred. No. 4;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDGKRIQDD 10
Db 281 EGGKEVQDD 290

RESULT 12

G84970
3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) [imported] - Buchnera sp. (C
C:Species: Buchnera sp.
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: G84970
R:Shigenobu, S.; Matanabe, H.; Hattori, M.; Sakai, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp
A:Reference number: A84930; MUID:20445173; PMID:10993077
A:Accession: G84970
A:Status: preliminary
A:Molecule type: DNA
A.Residues: 1-244 <STO>
A:Cross-references: GB:AP000398; GSPDB:GN00144
A:Experimental source: strain APS
C:Genetics:
A:Gene: fabG; EU351
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C:Keywords: oxidoreductase

Query Match 76.9%; Score 40; DB 2; Length 244;
Best Local Similarity 77.8%; Pred. No. 7.1;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDGKRIQDD 9
Db 39 EDGVRKIND 47

RESULT 13

T48951
hypothetical protein T1583.110 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
C:Accession: T48951
R:Jordan, N.; Bangerf, S.; Wiedemann, R.; Voss, H.; Unsel, M.; Mewes, H.W.; Rudd, S.;
submitted to the Protein Sequence Database, April 2000
A:Reference number: 225009
A:Accession: T48951
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-122 <JDR>
A:Cross-references: EMBL:AL63975; GSPDB:GN00061; ATSP:T15B3.110
A:Experimental source: cultivar Columbia; BAC clone T15B3
C:Genetics:
A:Gene: ATSP:T15B3.110
A:Map position: 3
A:Introns: 72/2
C:Superfamily: Arabidopsis thaliana hypothetical protein T15B3.110

Query Match 75.0%; Score 39; DB 2; Length 122;
Best Local Similarity 60.0%; Pred. No. 5.3;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDGIRRIODD 10
:|:|:|:|:|:|
Db 16 DGVRLRIODD 25

RESULT 14
G88124
protein nhr-16 [Imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: G88124
R:anonymous; The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.elg
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: G88124
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-387 <STD>
A:Cross-references: GB:chr.II; PIDN:AC71144.1; PID:93844613; GSPDB:GN00020; CESP:T12C9.1
C:Genetics:
A:Gene: nhr-16
A:Map position: 2

Query Match 73.1%; Score 38; DB 2; Length 387;
Best Local Similarity 60.0%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDGIRRIODD 10
:|:|:|:|:|:|
Db 354 QKGVRRRIODD 363

RESULT 15
T43355
nuclear receptor NHR-16 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
C:Accession: T43355
R:Sluder, A.E.; Mathews, S.W.; Hough, D.; Yin, V.P.; Maina, C.V.
Genome Res. 9, 103-120, 1999
A:Title: The nuclear receptor superfamily has undergone extensive proliferation and divergence
A:Reference number: 22443; MUID:99148134; PMID:10022975
A:Accession: T43355
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-388 <SLD>
A:Cross-references: EMBL:AF083231; NID:g4139087; PIDN:AAD03689.1; PID:g4139088
C:Genetics:

A:Gene: nhr-16
A:Map position: 2

Query Match 73.1%; Score 38; DB 2; Length 388;
Best Local Similarity 60.0%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDGIRRIODD 10
:|:|:|:|:|:|
Db 355 QKGVRRRIODD 364

Search completed: November 12, 2002, 16:17:52
Job time : 16 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:15:53 ; Search time 29 seconds
(without alignments)
71.051 Million cell updates/sec

Title: US-09-540-816-1
Perfect score: 52
Sequence: 1 EDGIRKIQDD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	343	11 09QW32	09QW32 rattus sp.
2	52	100.0	359	4 08TBK4	08TBK4 homo sapien
3	52	100.0	359	6 09GLN9	09GLN9 pan troglod
4	52	100.0	359	6 09N0U1	09N0U1 ovis aries
5	49	94.2	359	11 09EPP3	09EPP3 cavia porce
6	49	94.2	359	11 09EOR9	09EOR9 meriones un
7	44	84.6	359	10 09FLM8	09FLM8 arabidopsis
8	43	82.7	224	10 09LVO3	09LVO3 arabidopsis
9	43	82.7	359	10 09FIU9	09FIU9 arabidopsis
10	43	82.7	361	10 09FLN7	09FLN7 arabidopsis
11	42	80.8	326	2 046142	046142 clostridium
12	40	76.9	356	10 09FLI6	09FLI6 arabidopsis
13	40	76.9	360	10 09FIU8	09FIU8 arabidopsis
14	40	76.9	361	10 09FKI7	09FKI7 arabidopsis
15	40	76.9	362	10 09FLW7	09FLW7 arabidopsis
16	40	76.9	366	10 09LDH8	09LDH8 arabidopsis

17	40	76.9	834	10 09FEL2	09FEL2 arabidopsis
18	39	75.0	122	10 09LXW2	09LXW2 arabidopsis
19	39	75.0	184	12 09EN08	09EN08 amata moo
20	38	73.1	369	10 09FL68	09FL68 arabidopsis
21	38	73.1	1680	4 09P129	09P129 homo sapien
22	37	71.2	130	10 09FM36	09FM36 arabidopsis
23	37	71.2	367	5 046231	046231 drosophila
24	37	71.2	403	5 09VA56	09VA56 drosophila
25	37	71.2	538	16 08U449	08U449 agrobacteri
26	36	69.2	53	5 0950U2	0950U2 caenorhabdi
27	36	69.2	65	9 09T1H0	09T1H0 lactobacilli
28	36	69.2	190	5 09BH37	09BH37 drosophila
29	36	69.2	254	17 058498	058498 methanococc
30	36	69.2	317	5 097338	097338 physarum po
31	36	69.2	341	16 092DD0	092DD0 listeria in
32	36	69.2	342	16 08Y8X3	08Y8X3 listeria mo
33	36	69.2	368	10 09LSR0	09LSR0 arabidopsis
34	36	69.2	384	10 093699	093699 vigna ungu
35	36	69.2	417	2 050201	050201 streptococc
36	36	69.2	442	5 09V4A0	09V4A0 drosophila
37	36	69.2	464	17 058649	058649 pyrococcus
38	36	69.2	465	17 09UZB9	09UZB9 pyrococcus
39	36	69.2	531	16 098B30	098B30 thizobium 1
40	36	69.2	563	5 09VAH5	09VAH5 drosophila
41	36	69.2	595	5 09NBW7	09NBW7 drosophila
42	36	69.2	615	5 091573	091573 caenorhabdi
43	36	69.2	650	5 09G201	09G201 plasmodium
44	36	69.2	672	5 09U0K1	09U0K1 plasmodium
45	36	69.2	1623	4 060303	060303 homo sapien

ALIGNMENTS

RESULT 1
ID 09QW32 PRELIMINARY; PRT; 343 AA.
AC 09QW32;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Angiotensin receptor Atr1.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93176370; PubMed=1290618;
RA Murphy T.J., Takeuchi K., Alexander R.W.;
RT "Molecular cloning of Atr1 angiotensin receptors.";
RL Am. J. Hypertens. 5:236-236(1992).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR HSSP: P34996; 1DDP.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSN.
DR PROSITE: PS00237; G-PROTEIN_RECPEP_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECPEP_F1_2; 1.
KW G-protein coupled receptor; glycoprotein; Transmembrane.
SQ SEQUENCE 343 AA; 39155 MW; 2CC6A22004CC93C CRC64;

Query Match 100.0%; Score 52; DB 11; Length 343;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGIRKIQDD 10
|||||
DB 6 EDGIRKIQDD 15

RESULT 2

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O8TBK4
ID O8TBK4 PRELIMINARY; PRT; 359 AA.
AC O8TBK4:
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Angiotensin receptor 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022447; AAH22447.1; -.
KW Receptor.
SQ SEQUENCE 359 AA; 41087 MW; AF90BE7F21E911BA CRC64;

Query Match
Best Local Similarity 100.0%; Score 52; DB 4; Length 359;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGIKRIQDD 10
DB 8 EDGIKRIQDD 17

RESULT 3
O9GLN9
ID O9GLN9 PRELIMINARY; PRT; 359 AA.
AC O9GLN9:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Angiotensin II type-1 receptor.
GN AGTRL.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20469400; PubMed=11013071;
RA Dufour C., Casane D., Denton D., Wickings J., Corvol P.,
RA Jeunemaitre X.;
RT "Human-Chimpanzee DNA sequence variation in the four major genes of
RT the renin angiotensin system.";
RL Genomics 69:14-26(2000).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF193445; AAG28410.1; -.
DR HSSP; P34996; 1DD.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_REC_P1.1; 1.
DR PROSITE; PS0262; G_PROTEIN_REC_P1.2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 359 AA; 41033 MW; 266133A7A3E911A6 CRC64;

Query Match
Best Local Similarity 100.0%; Score 52; DB 6; Length 359;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGIKRIQDD 10
DB 8 EDGIKRIQDD 17

RESULT 4
O9NOU1
ID O9NOU1 PRELIMINARY; PRT; 359 AA.
AC O9NOU1:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Angiotensin II type 1 receptor.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ADRENAL CORTEX;
RA Bird I.M., Milligan D.S.;
RT "Isolation of a full length ovine Angiotensin II Type-1 Receptor (AT1-
RT R) cDNA.";
RL Endocr. Res. 0:0-0(2000).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF254119; AAF66063.1; -.
DR HSSP; P34996; 1DD.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_REC_P1.1; 1.
DR PROSITE; PS0262; G_PROTEIN_REC_P1.2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 359 AA; 41062 MW; C07010EDB81110EB CRC64;

Query Match
Best Local Similarity 100.0%; Score 52; DB 6; Length 359;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGIKRIQDD 10
DB 8 EDGIKRIQDD 17

RESULT 5
O9EPP3
ID O9EPP3 PRELIMINARY; PRT; 359 AA.
AC O9EPP3:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Angiotensin II type 1 receptor.
GN ATL1.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=GALL BLADDER;
RA Busmann A., Noack T., Zucht HD., Forssmann W.G., Meyer M.;
RT "Isolation of Angiotensin I from human hemofiltrate as a potent
RT modulator of K+ channels.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ301623; CAC21550.1; -.
DR HSSP; P34996; 1DD.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_REC_P1.1; 1.
DR PROSITE; PS0262; G_PROTEIN_REC_P1.2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 359 AA; 41045 MW; D00F4C2472DE5CC CRC64;

Query Match
Best Local Similarity 94.2%; Score 49; DB 11; Length 359;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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ID O9NOU1 PRELIMINARY; PRT; 359 AA.
AC O9NOU1:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Angiotensin II type 1 receptor.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ADRENAL CORTEX;
RA Bird I.M., Milligan D.S.;
RT "Isolation of a full length ovine Angiotensin II Type-1 Receptor (AT1-
RT R) cDNA.";
RL Endocr. Res. 0:0-0(2000).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF254119; AAF66063.1; -.
DR HSSP; P34996; 1DD.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_REC_P1.1; 1.
DR PROSITE; PS0262; G_PROTEIN_REC_P1.2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 359 AA; 41062 MW; C07010EDB81110EB CRC64;

Query Match
Best Local Similarity 100.0%; Score 52; DB 6; Length 359;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGIKRIQDD 10
DB 8 EDGIKRIQDD 17

RESULT 5
O9EPP3
ID O9EPP3 PRELIMINARY; PRT; 359 AA.
AC O9EPP3:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Angiotensin II type 1 receptor.
GN ATL1.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=GALL BLADDER;
RA Busmann A., Noack T., Zucht HD., Forssmann W.G., Meyer M.;
RT "Isolation of Angiotensin I from human hemofiltrate as a potent
RT modulator of K+ channels.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ301623; CAC21550.1; -.
DR HSSP; P34996; 1DD.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_REC_P1.1; 1.
DR PROSITE; PS0262; G_PROTEIN_REC_P1.2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 359 AA; 41045 MW; D00F4C2472DE5CC CRC64;

Query Match
Best Local Similarity 94.2%; Score 49; DB 11; Length 359;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGIRRIODD 10
 :|||||
 DB 8 ODGIRRIODD 17

RESULT 6

O9EOR9 PRELIMINARY: PRT: 359 AA.

AC O9EOR9; PRELIMINARY: PRT: 359 AA.
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Angiotensin II receptor type 1B.
 GN AT1B.
 OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
 OC Meriones.
 OX NCBI_TaxID=10047;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-ADRENAL GLAND;
 RA Hoe K.-L., Saavedra J.M.;
 RT "Molecular cloning and pharmacological characterization of an atypical
 gerbil angiotensin II type-1 receptor and amino acids which are
 important in Losartan binding."
 RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 DR EMBL: AF078794; AAG3172.1; -.
 DR HSSP: P34996; 1DDD
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PS00237; GPCR_RHODOPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 SQ SEQUENCE 359 AA; 40934 MW; 3FA1CCECB73AA29 CRC64;

Query Match 94.2%; Score 49; DB 11; Length 359;
 Best Local Similarity 90.0%; Pred. No. 0.65;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGIRRIODD 10
 :|||||
 DB 8 EDGIRRIODD 17

RESULT 7

O9FLW8 PRELIMINARY: PRT: 359 AA.

AC O9FLW8; PRELIMINARY: PRT: 359 AA.
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Genomic DNA, chromosome 5, p1 clone:MXC20.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RX MEDLINE=98290546; PubMed=9628582;
 RA Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.
 RT Sequence features of the regions of 1,456,315 bp covered by nineteen
 RT physically assigned P1 and TAC clones.";
 RL DNA Res. 5:41-54(1998).

DR EMBL: AB009055; BAB10441.1; -.
 DR InterPro: IPR005174; DUF295.
 DR Pfam: PF03478; DUF295; 1.
 SQ SEQUENCE 359 AA; 39689 MW; 6F961096FCB25DD9 CRC64;

Query Match 84.6%; Score 44; DB 10; Length 359;
 Best Local Similarity 80.0%; Pred. No. 5.4;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDGIRRIODD 10
 :|||||
 DB 93 EDGIRRIODD 102

RESULT 8

O9LV03 PRELIMINARY: PRT: 224 AA.

AC O9LV03; PRELIMINARY: PRT: 224 AA.
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Genomic DNA, chromosome 5, p1 clone:MWJ3.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RX MEDLINE=20181125; PubMed=10718197;
 RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
 RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
 RT clones."
 RL DNA Res. 7:31-63(2000).
 DR EMBL: AB018120; BAA97286.1; -.
 DR InterPro: IPR005174; DUF295.
 DR Pfam: PF03478; DUF295; 1.
 SQ SEQUENCE 224 AA; 25814 MW; AED2A3FAD0295D95 CRC64;

Query Match 82.7%; Score 43; DB 10; Length 224;
 Best Local Similarity 80.0%; Pred. No. 5;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDGIRRIODD 10
 :|||||
 DB 87 EDGIRRIODD 96

RESULT 9

O9FTU9 PRELIMINARY: PRT: 359 AA.

AC O9FTU9; PRELIMINARY: PRT: 359 AA.
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Genomic DNA, chromosome 5, p1 clone:MRB17.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RX MEDLINE=99087489; PubMed=9872454;
 RA Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VII.
 RT Sequence features of the regions of 1,013,767 bp covered by sixteen
 RT physically assigned P1 and TAC clones.";

RL DNA Res. 5:297-308(1998).
 DR EMBL: AB016879; BAB09334.1; -
 DR InterPro: IPR005174; DUF295.
 DR Pfam: PF03478; DUF295; 1.
 SQ SEQUENCE 359 AA; 39959 MW; 5D64DB36253BBD2E CRC64;

Query Match
 Best Local Similarity 82.7%; Score 43; DB 10; Length 359;
 Pred. No. 8.2;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDGIRRIQDD 10
 ||||| :|||
 Db 97 EDGIRLRQDD 106

RESULT 10

O9FLN7 PRELIMINARY; PRT; 361 AA.
 AC O9FLN7;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Genomic DNA, chromosome 5, pl clone:MC015.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=98290546; PubMed=9628582;
 RA Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.
 RT Sequence features of the regions of 1,456,315 bp covered by nineteen
 RT physically assigned pl and TAC clones.";
 RL DNA Res. 5:41-54(1998).
 DR EMBL: AB010071; BAB08596.1; -
 DR InterPro: IPR005174; DUF295.
 DR Pfam: PF03478; DUF295; 1.
 SQ SEQUENCE 361 AA; 40320 MW; 61F2616083455B90 CRC64;

Query Match
 Best Local Similarity 82.7%; Score 43; DB 10; Length 361;
 Pred. No. 8.3;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDGIRRIQDD 10
 ||||| :|||
 Db 96 EDGIRLRQDD 105

RESULT 11

O46142 PRELIMINARY; PRT; 326 AA.
 AC O46142;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE TPP-dependent acetoin dehydrogenase alpha-subunit.
 OS Clostridium magnum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiaceae; Clostridium.
 OX NCBI_TaxID=33954;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WO BD P1;
 RX MEDLINE=94266715; PubMed=8206840;
 RA Kruger N., Oppermann F.B., Lorenz H., Steinbuechel A.;
 RT "Biochemical and molecular characterization of the Clostridium magnum
 RT acetoin dehydrogenase enzyme system [published erratum appears in J
 RT Bacteriol. 1994 Aug;176(16):5193].";
 RL J. Bacteriol. 176:3614-3630(1994).

DR EMBL: L31844; AAA21744.1; -
 DR InterPro: IPR001017; Dehydrogenase_E1.
 DR Pfam: PF00676; E1_dehydrog; 1.
 SQ SEQUENCE 326 AA; 35573 MW; 1EBB813B5444801 CRC64;

Query Match
 Best Local Similarity 80.8%; Score 42; DB 2; Length 326;
 Pred. No. 11;
 Matches 7; Conservative .2; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDGIRRIQDD 10
 ||||| :|||
 Db 281 EGGIKRQDD 290

RESULT 12

O9FL67 PRELIMINARY; PRT; 356 AA.
 AC O9FL67;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Genomic DNA, chromosome 5, pl clone:MDK4.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=98344145; PubMed=9679202;
 RA Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence
 RT features of the regions of 1,381,565 bp covered by twenty one
 RT physically assigned pl and TAC clones.";
 RL DNA Res. 5:131-145(1998).
 DR EMBL: AB010695; BAB10756.1; -
 DR InterPro: IPR005174; DUF295.
 DR Pfam: PF03478; DUF295; 1.
 SQ SEQUENCE 356 AA; 39703 MW; 283DEB9743339E64 CRC64;

Query Match
 Best Local Similarity 76.9%; Score 40; DB 10; Length 356;
 Pred. No. 29;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDGIRRIQDD 10
 ||||| :|||
 Db 87 DDGIRLRQDD 96

RESULT 13

O9FL08 PRELIMINARY; PRT; 360 AA.
 AC O9FL08;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Genomic DNA, chromosome 5, pl clone:WRB17.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=99087489; PubMed=9872454;
 RA Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VII.
 RT Sequence features of the regions of 1,013,767 bp covered by sixteen
 RT physically assigned pl and TAC clones.";

RL DNA Res. 5:257-308(1998).
DR EMBL: AB016879; BAB09335.1; -
DR InterPro: IPR005174; DUF295.
DR Pfam: PF03478; DUF295; 1.
SQ SEQUENCE 360 AA; 40036 MW; FA307E30630E9C29 CRC64;

Query Match 76.9%; Score 40; DB 10; Length 360;
Best Local Similarity 70.0%; Pred. No. 29;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDGIRRIODD 10
:|||||:
DB 99 DDGIRLRLODD 108

RESULT 14

O9FKI7 PRELIMINARY; PRT; 361 AA.
AC O9FKI7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Genomic DNA, chromosome 5, TAC clone:K19E1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RX MEDLINE=98403884; PubMed=9734815;
RA Kocani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
RT Sequence features of the regions of 1,367,185 bp covered by 19
RL DNA Res. 5:203-216(1998).
DR EMBL: AB013388; BAB09786.1; -
DR InterPro: IPR005174; DUF295.
DR Pfam: PF03478; DUF295; 1.
SQ SEQUENCE 361 AA; 40494 MW; CC045013827EE88A CRC64;

Query Match 76.9%; Score 40; DB 10; Length 361;
Best Local Similarity 70.0%; Pred. No. 30;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDGIRRIODD 10
:|||||:
DB 89 DDGIRLRLODD 98

RESULT 15

O9FLW7 PRELIMINARY; PRT; 362 AA.
AC O9FLW7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Genomic DNA, chromosome 5, PI clone:MXC20.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RX MEDLINE=98290546; PubMed=9628582;
RA Sato S., Kaneko T., Kocani H., Nakamura Y., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.
RT Sequence features of the regions of 1,456,315 bp covered by nineteen

RT physically assigned PI and TAC clones.";
RL DNA Res. 5:41-54(1998).
DR EMBL: AB009055; BAB10442.1; -
DR InterPro: IPR005174; DUF295.
DR Pfam: PF03478; DUF295; 1.
DR PROSITE: PS00092; N6_MTASE; UNKNOWN_1.
SQ SEQUENCE 362 AA; 40352 MW; 630B74E8FC0A1A69 CRC64;

Query Match 76.9%; Score 40; DB 10; Length 362;
Best Local Similarity 70.0%; Pred. No. 30;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDGIRRIODD 10
:|||||:
DB 96 DDGIRLRLODD 105

Search completed: November 12, 2002, 16:16:31
Job time : 31 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:15:53 ; Search time 10 Seconds
(without alignments)
41.476 Million cell updates/sec

Title: US-09-540-816-1
Perfect score: 52
Sequence: 1 EDCIKRIODD 10

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	359	1 AG2R_BOVIN	P25104 Bos taurus
2	52	100.0	359	1 AG2R_CANFA	P43240 canis fam1
3	52	100.0	359	1 AG2R_CAVPO	Q9WV26 canis porce
4	52	100.0	359	1 AG2R_HUMAN	P30556 homo sapien
5	52	100.0	359	1 AG2R_MOUSE	P29754 mus musculu
6	52	100.0	359	1 AG2R_RABIT	P34976 oryctolagus
7	52	100.0	359	1 AG2R_RAT	P25095 rattus norv
8	52	100.0	359	1 AG2R_SHEEP	O77590 ovis aries
9	52	100.0	359	1 AG2S_HUMAN	Q13725 homo sapien
10	52	100.0	359	1 AG2S_MOUSE	P29755 mus musculu
11	52	100.0	359	1 AG2S_RAT	P29089 rattus norv
12	49	94.2	359	1 AG2R_MERUN	O35210 meriones un
13	46	88.5	359	1 AG2R_PIG	P30535 sus scrofa
14	40	76.9	244	1 FABG_BUCAI	P37432 buchnera ap
15	38	73.1	388	1 NH16_CAEEL	Q27521 caenorhabdi
16	36	69.2	130	1 RL22_CAEEL	P52819 caenorhabdi
17	36	69.2	443	1 HSLU_VIRCH	Q9Kng7 vibrio chol
18	36	69.2	595	1 FRA_DROME	P21525 drosophila
19	35	67.3	174	1 NADM_ARCFU	O27966 archaeoglob
20	35	67.3	288	1 Y940_MYCTU	P71559 mycobacteri
21	35	67.3	342	1 K6P1_STRMY	O08333 streptomyce
22	34	65.4	184	1 RRF_BORBU	O31147 borrelia bu
23	34	65.4	291	1 DLHH_MEREX	P71505 methyllobact
24	34	65.4	375	1 DNAJ_ACTAC	P77866 actinobacill
25	34	65.4	377	1 DNAJ_BUCAI	O32465 buchnera ap
26	34	65.4	392	1 TEBB_STYMY	P29548 stylyomyia
27	34	65.4	447	1 HSLU_PSEAE	Q38065 pseudomonas
28	34	65.4	501	1 YB06_YEAST	P38061 saccharomyc
29	34	65.4	866	1 MCM4_DROME	O26454 drosophila
30	34	65.4	3390	1 POLG_DEN3	P27915 d genome po
31	33	63.5	198	1 RECR_BACHD	Q9Kgm1 bacillus ha
32	33	63.5	198	1 RECR_LISIN	Q92749 listeria in
33	33	63.5	198	1 RECR_LISMO	O9Y347 listeria mo

34	33	63.5	222	1 TDXH_AQUAE	O67024 aquifex aeo
35	33	63.5	232	1 ISPD_BACSU	O06755 bacillus su
36	33	63.5	280	1 SPEED_AQUAE	O66473 aquifex aeo
37	33	63.5	313	1 GAS2_HUMAN	O43903 homo sapien
38	33	63.5	314	1 GAS2_MOUSE	P41862 mus musculu
39	33	63.5	347	1 YN24_CAEEL	P4583 caenorhabdi
40	33	63.5	387	1 THII_MYCPN	P75228 mycoplasma
41	33	63.5	459	1 RBL2_THIDE	O60028 thibobacillu
42	33	63.5	491	1 GAT1_STRPN	O97p15 streptococc
43	33	63.5	503	1 YPTJ_CAEEL	Q23469 caenorhabdi
44	33	63.5	551	1 REFR_VACCV	P04321 vaccinia vi
45	33	63.5	551	1 REFR_VARY	P33810 variola vir

ALIGNMENTS

RESULT 1	AG2R_BOVIN	STANDARD:	PRT:	359 AA.
AC	P25104:			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-MAY-1992 (Rel. 22, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	Type-1 angiotensin II receptor (AT1).			
GN	AGRI.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_Taxid=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-91251900; PubMed-2041569;			
RA	Sasaki K., Yamano Y., Barchan S., Iwai N., Murray J.J., Hasegawa M.,			
RA	Matsuda Y., Inagami T.;			
RT	*Cloning and expression of a complementary DNA encoding a bovine			
RT	adrenal angiotensin II type-1 receptor.;"			
RL	Nature 351:230-233(1991).			
CC	-1- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY			
CC	ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-			
CC	CALCIUM SECOND MESSENGER SYSTEM.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- TISSUE SPECIFICITY: ADRENAL MEDULLA, CORTEX, AND KIDNEY.			
CC	-1- PFM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	-----			
DR	EMBL: X62294; CAA44182.1; -			
DR	PIR: S15403; S15403.			
DR	HSSP: P34996; IIDD.			
DR	InterPro: IPR000276; GPCR_Rhodpsn.			
DR	PIfam: PFM0001; 7tm_1; 1.			
DR	PRINTS: PR00237; GPCRHHODPSN.			
DR	PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.			
DR	PROSITE: PS50262; G-PROTEIN_RECEP_FL_2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;			
KW	Palmitate; Phosphorylation.			
FT	DOMAIN 1 27			
FT	TRANSMEM 28 52			
FT	DOMAIN 53 64			
FT	TRANSMEM 65 87			
FT	DOMAIN 88 102			
FT	TRANSMEM 103 124			
FT	DOMAIN 125 142			
FT	TRANSMEM 143 162			
FT	-----			
FT	EXTRACELLULAR (POTENTIAL).			
FT	CYTOPLASMIC (POTENTIAL).			
FT	2 (POTENTIAL).			
FT	EXTRACELLULAR (POTENTIAL).			
FT	3 (POTENTIAL).			
FT	CYTOPLASMIC (POTENTIAL).			
FT	4 (POTENTIAL).			

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FT DOMAIN 163 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 214 5 (POTENTIAL).
FT DOMAIN 215 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 241 262 6 (POTENTIAL).
FT DOMAIN 263 275 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 296 7 (POTENTIAL).
FT DOMAIN 297 359 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 101 180 BY SIMILARITY.
FT LIPID 355 355 PALMITATE (POTENTIAL).
SQ SEQUENCE 359 AA; 41088 MW; B426BFF6B61DFF6A CRC64;

Query Match 100.0%; Score 52; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGIRRIODD 10
Db 8 EDGIRRIODD 17

RESULT 2
AG2R_CANFA STANDARD; PRT; 359 AA.
ID AG2R_CANFA
AC P43240;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Type-1 angiotensin II receptor (AT1).
GN AGTRL.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxId=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94222186; PubMed=8168620;
RA Burns L., Clark K.L., Bradley J., Robertson M.J., Clark A.J.;
RT "Molecular cloning of the canine angiotensin II receptor. An AT1-like
RL receptor with reduced affinity for Dnp753."
RL FEBS Lett. 343:146-150(1994).
CC -1- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: ADRENAL, LIVER, AORTA, KIDNEY, LUNG, TESTIS
CC AND HEART.
CC -1- PM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR HSSP: P34996. 1DD.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSN.
DR PROSITE: PS00237; G-PROTEIN_RECP_FL_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
KW Palmitate; Phosphorylation.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 52 1 (POTENTIAL).
FT DOMAIN 53 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 87 2 (POTENTIAL).
FT DOMAIN 88 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 142 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 143 162 4 (POTENTIAL).
FT DOMAIN 163 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 214 5 (POTENTIAL).
FT DOMAIN 215 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 241 262 6 (POTENTIAL).
FT DOMAIN 263 275 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 276 296 7 (POTENTIAL).
FT DOMAIN 297 359 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 101 180 BY SIMILARITY.
FT LIPID 355 355 PALMITATE (POTENTIAL).
SQ SEQUENCE 359 AA; 40901 MW; 22A1BADFA8D50E CRC64;

Query Match 100.0%; Score 52; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGIRRIODD 10
Db 8 EDGIRRIODD 17

RESULT 3
AG2R_CAVPO STANDARD; PRT; 359 AA.
ID AG2R_CAVPO
AC O9WV26;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Type-1 angiotensin II receptor (AT1).
GN AGTRL.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
OX NCBI_TaxId=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley; TISSUE=Liver;
RX MEDLINE=20423173; PubMed=10965057;
RA Hosoda Y., Fujino I., Akagawa K., Kuwahara A.;
RT "Molecular cloning of guinea pig angiotensin type 1 receptor."
RL Biol. Signals Recept. 9:231-239(2000).
CC -1- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- PM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF165888; AAD45383.1; -.
DR HSSP: P34996. 1DD.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSN.
DR PROSITE: PS00237; G-PROTEIN_RECP_FL_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
KW Palmitate; Phosphorylation.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 52 1 (POTENTIAL).
FT DOMAIN 53 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 87 2 (POTENTIAL).
FT DOMAIN 88 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 142 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 143 162 4 (POTENTIAL).
FT DOMAIN 163 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 214 5 (POTENTIAL).
FT DOMAIN 215 240 CYTOPLASMIC (POTENTIAL).

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FT TRANSMEM 241 262 6 (POTENTIAL).
FT DOMAIN 263 275 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 296 7 (POTENTIAL).
FT DOMAIN 297 359 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 101 180 BY SIMILARITY.
FT LIPID 355 355 PALMITATE (POTENTIAL).
SQ SEQUENCE 359 AA; 40985 MW; 11991138F9F81C19 CRC64;

Query Match 100.0%; Score 52; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGIRIQQD 10
DB 8 EDGIRIQQD 17

RESULT 4
AG2R_HUMAN
ID AG2R_HUMAN STANDARD; PRT; 359 AA.
AC P30556;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Type-1 angiotensin II receptor (AT1) (A11AR).
GN AGTR1 OR AGTR1A OR AT2RL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=92337608; PubMed=1378723;
RA Manzy C.A., Hwang O., Ejlöf A.M., Wu L.H., Chung F.-Z.;
RT "Cloning, expression, and characterization of a gene encoding the
RL human angiotensin II type 1A receptor."
RN Biochem. Biophys. Res. Commun. 186:277-284(1992).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes;
RC MEDLINE=92181475; PubMed=1543512;
RA Furuta H., Guo D.F., Inagami T.;
RT "Molecular cloning and sequencing of the gene encoding human
RL angiotensin II type 1 receptor."
RN Biochem. Biophys. Res. Commun. 183:8-13(1992).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RC MEDLINE=92231907; PubMed=1567413;
RA Bergsma D.J., Ellis C., Kumar C., Nuthalaganti P., Kersten H.,
RA Elsinouday N.A., Griffin E., Stadel J.M., Aiyer N.;
RT "Cloning and characterization of a human angiotensin II type 1
RL receptor."
RN Biochem. Biophys. Res. Commun. 183:989-995(1992).
[4]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RC MEDLINE=92198490; PubMed=1550596;
RA Takayanagi R., Ohnaka K., Sakai Y., Nakao R., Yanase T., Hagi M.,
RA Inagami T., Furuta H., Gou D.F., Nakamura M., Nawata H.;
RT "Molecular cloning, sequence analysis and expression of a cDNA
RL encoding human type-1 angiotensin II receptor."
RN Biochem. Biophys. Res. Commun. 183:910-916(1992).
[5]
RP SEQUENCE FROM N.A.
RC MEDLINE=92375105; PubMed=1508224;
RA Currow K.M., Pascoe L., White P.C.;
RT "Genetic analysis of the human type-1 angiotensin II receptor."
RN Mol. Endocrinol. 6:1113-1118(1992).
[6]

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RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RC MEDLINE=95313084; PubMed=7792812;
RX Nawata H., Takayanagi R., Ohnaka K., Sakai Y., Imasaki K., Yanase T.,
RA Ikuyama S., Tanaka S., Ohe K.;
RT "Type 1 angiotensin II receptors of adrenal tumors."
RL Steroids 60:28-34(1995).
[7]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Ostermann E., Castanon M.J.;
RN Submitted (xxx-1995) to the EMBL/GenBank/DBJ databases.
[8]
RP SEQUENCE FROM N.A.
RA Antonellis A., Rogus J.J., Perzolesi M.G., Makita Y., Nam M.,
RA Doria A., Warram J.H., Krolewski A.S.;
RT "Rapid identification of polymorphisms in genomic DNA: a high density
RT SNP map of the type 1 angiotensin II receptor gene locus on chromosome
RT 3q."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - TISSUE SPECIFICITY: LIVER, LUNG, ADRENAL, AND ADRENOCORTICAL
CC ADENOMAS.
CC - PKM: CARBOXY-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL: M91464; AAA5569.1; -
DR EMBL: Z11162; AAA7513.1; -
DR EMBL: M87290; AAA35535.1; -
DR EMBL: M93394; AAA58370.1; -
DR EMBL: S77410; AAB34644.1; -
DR EMBL: X65699; CAA46621.1; -
DR EMBL: AF245699; AAF70464.1; -
DR PIR: A44014; A44014.
DR PIR: JC1104; JC1104.
DR HSSP: P34996; 1DD.
DR GeneW: HGNC:336; AGTR1.
DR MIM: 106165; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE: PS02662; G_PROTEIN_RECPT_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
KW Palmitate; Phosphorylation; Polymorphism.
FT DOMAIN 1 27
FT TRANSMEM 28 52
FT DOMAIN 53 64
FT TRANSMEM 65 87
FT DOMAIN 88 102
FT TRANSMEM 103 124
FT DOMAIN 125 142
FT TRANSMEM 143 162
FT DOMAIN 163 192
FT TRANSMEM 193 214
FT DOMAIN 215 240
FT TRANSMEM 241 262
FT DOMAIN 263 275
FT TRANSMEM 276 296
FT DOMAIN 297 359
FT CARBOHYD 4 4
FT CARBOHYD 176 176

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FT CAROHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 101 180 BY SIMILARITY.
FT LIPID 355 355 PALMITATE (POTENTIAL).
FT VARIANT 48 48 L-> V (IN DBSNP:2011425).
FT VARIANT 289 289 C-> W (IN DBSNP:1064533).
FT VARIANT 289 289 /FTID=VAR_011847.
FT VARIANT 336 336 /FTID=VAR_011847.
FT VARIANT 336 336 /FTID=VAR_011848.
FT VARIANT 336 336 /FTID=VAR_1801021.
SQ SEQUENCE 359 AA; 41061 MW; 35FC856F53E911A6 CRC64;

Query Match 100.0%; Score 52; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDGIRKRIQDD 10
Db 8 EDGIRKRIQDD 17

RESULT 5
AG2R_MOUSE STANDARD; PRT; 359 AA.
AC P29754:
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Type-1A angiotensin II receptor (AT1A).
GN AGT1A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAIB/C; TISSUE=Liver;
RX MEDLINE=92287102; PubMed=1599461;
RA Sasamura H., Hein L., Krieger J.E., Pratt R.E., Kobilka B.K.,
RA Dzu V.J.;
RT "Cloning, characterization, and expression of two angiotensin
RL receptor (AT-1) isoforms from the mouse genome.";
RL Biochem. Biophys. Res. Commun. 185:253-259(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92359981; PubMed=1497638;
RA Yoshida H., Kakuchi J., Guo D.F., Furuta H., Iwai N.,
RA van der Meer-De Jong R., Inagami T., Ichikawa T.;
RT "Analysis of the evolution of angiotensin II type 1 receptor gene in
RL mammals (mouse, rat, bovine and human).";
RL Biochem. Biophys. Res. Commun. 186:1042-1049(1992).
CC -1- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- PM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO FAMILY I OF G-PROTEIN COUPLED RECEPTORS.
CC -1- SIMILARITY: BELONGS TO FAMILY I OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
CC EMBL: S37484; AAB22269.1; -.
CC PIR: JH0621; JH0621.
CC PIR: JC1193; JC1193.
CC HSSP: P34996; 1DDO.
CC MGD: MGI:87964; Agt1a.
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam: PF00001; 7tm_1; 1.
CC PRINTS: PR00237; GPCR_RHODOPSN.

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DR PROSITE: PS00237; G-PROTEIN_REC_P1_1; 1.
DR PROSITE: PS00262; G-PROTEIN_REC_P1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
KW Palmitate; Phosphorylation.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 52 1 (POTENTIAL).
FT DOMAIN 53 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 87 2 (POTENTIAL).
FT DOMAIN 88 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 142 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 143 162 4 (POTENTIAL).
FT TRANSMEM 163 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 214 5 (POTENTIAL).
FT DOMAIN 215 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 241 262 6 (POTENTIAL).
FT DOMAIN 263 275 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 296 7 (POTENTIAL).
FT DOMAIN 297 359 CYTOPLASMIC (POTENTIAL).
FT CAROHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 101 180 BY SIMILARITY.
FT LIPID 355 355 PALMITATE (POTENTIAL).
FT CONFLICT 7 7 T-> I (IN REF. 2).
FT CONFLICT 20 21 RA-> IS (IN REF. 2).
FT CONFLICT 38 38 I-> M (IN REF. 2).
FT CONFLICT 134 134 M-> K (IN REF. 2).
SQ SEQUENCE 359 AA; 40855 MW; 966958A738D8F53E CRC64;

Query Match 100.0%; Score 52; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDGIRKRIQDD 10
Db 8 EDGIRKRIQDD 17

RESULT 6
AG2R_RABIT STANDARD; PRT; 359 AA.
ID AG2R_RABIT
AC P34976:
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Type-1 angiotensin II receptor (AT1).
GN AGT1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93236091; PubMed=7916579;
RA Burns K.D., Inagami T., Harris R.C.;
RT "Cloning of a rabbit kidney cortex AT1 angiotensin II receptor that
RL is present in proximal tubule epithelium.";
RL Am. J. Physiol. 264:F645-F654(1993).
CC -1- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- PM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO FAMILY I OF G-PROTEIN COUPLED RECEPTORS.
CC -1- SIMILARITY: BELONGS TO FAMILY I OF G-PROTEIN COUPLED RECEPTORS.
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CC EMBL: S59041; AAB26239.1; -
DR PIR: A48857; A48857.
DR HSSE: P34996; 1DD.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PS00237; GPCR_HODOPS_N.
DR PROSITE: PS00237; G-PROTEIN_REC_P1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_REC_P1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
KW Palmitate; Phosphorylation.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 52 1 (POTENTIAL).
FT TRANSMEM 53 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 87 2 (POTENTIAL).
FT TRANSMEM 88 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT TRANSMEM 125 142 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 143 162 4 (POTENTIAL).
FT TRANSMEM 163 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 214 5 (POTENTIAL).
FT TRANSMEM 215 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 241 262 6 (POTENTIAL).
FT TRANSMEM 263 275 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 296 7 (POTENTIAL).
FT TRANSMEM 297 359 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT DISULFID 101 180 BY SIMILARITY.
FT LIPID 355 PALMITATE (POTENTIAL).
SQ SEQUENCE 359 AA; 40989 MM; C27AC1A2BB6AD576 CAC64;

Query Match 100.0%; Score 52; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGIRKRIODD 10
DB 8 EDGIRKRIODD 17

RESULT 7
AG2R_RAT STANDARD: PRT: 359 AA.
AC AG2R_RAT STANDARD: PRT: 359 AA.
AC P25095; G9QV55;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Type-1a angiotensin II receptor (AT1A).
GN AGT1A OR AT1A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Vascular smooth muscle;
RA MEDLINE=91251901; PubMed=2041570;
RA Murphy T.J., Alexander R.W., Griendling K.K., Runge M.S.,
RA Bernstein K.E.;
RT "Isolation of a cDNA encoding the vascular type-1 angiotensin II
RT receptor.";
RL Nature 351:233-236(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA MEDLINE=91254291; PubMed=2043116;
RA Iwai N., Yamano Y., Chaki S., Konishi F., Bardhan S., Tibbetts C.,
RA Sasaki K., Hasegawa M., Matsuda Y., Inagami T.;
RT "Rat angiotensin II receptor: cDNA sequence and regulation of the
RT gene expression.";

RL Biochem. Biophys. Res. Commun. 177:299-304(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92231859; PubMed=1533121;
RA Langford K.G., Frenzel K., Martin B.M., Bernstein K.E.;
RT "The genomic organization of the rat AT1 angiotensin receptor.";
RL Biochem. Biophys. Res. Commun. 183:1025-1032(1992).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=95228708; PubMed=7713098;
RA Inagami T., Iwai N., Sasaki K., Yamano Y., Bardhan S., Chaki S.,
RA Guo D.F., Furuta H., Ohyama K., Kamayashi Y.;
RT "Cloning, expression and regulation of angiotensin II receptors.";
RL Eur. J. 15:104-107(1994).
CC -1- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G-PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: IS EXPRESSED IN THE LIVER, KIDNEY, AORTA,
CC LUNG, UTERUS, OVARY, SPLEEN, HEART, ADRENAL GLAND, AND VASCULAR
CC SMOOTH MUSCLE CELL.
CC -1- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL: X62295; CAA4183.1; -
DR EMBL: M74054; AAA40738.1; -
DR EMBL: M86912; -; NOT_ANNOTATED_CDS.
DR PIR: JQ1055; JQ1055.
DR PIR: S15404; S15404.
DR PIR: S20424; S20424.
DR PIR: JC2134; JC2134.
DR HSSE: P34996; 1DD.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PS00237; GPCR_HODOPS_N.
DR PROSITE: PS00237; G-PROTEIN_REC_P1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_REC_P1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
KW Palmitate; Phosphorylation.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 52 1 (POTENTIAL).
FT TRANSMEM 53 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 87 2 (POTENTIAL).
FT TRANSMEM 88 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT TRANSMEM 125 142 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 143 162 4 (POTENTIAL).
FT TRANSMEM 163 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 214 5 (POTENTIAL).
FT TRANSMEM 215 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 241 262 6 (POTENTIAL).
FT TRANSMEM 263 275 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 296 7 (POTENTIAL).
FT TRANSMEM 297 359 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT DISULFID 101 180 BY SIMILARITY.
FT LIPID 355 PALMITATE (POTENTIAL).
FT LIPID 355 L->C (IN REF. 2).
FT CONFLICT 81 109 S->T (IN REF. 2 AND 4).
SQ SEQUENCE 359 AA; 40989 MM; 200EA55DB4DA678 CAC64;

Query Match 100.0%; Score 52; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.028;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGIRRIODD 10
 |||||||
 Db 8 EDGIRRIODD 17

RESULT 8
 AG2R_SHEEP STANDARD: PRT: 359 AA.
 ID AG2R_SHEEP STANDARD: PRT: 359 AA.
 AC 077590:
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Type-1 angiotensin II receptor (AT1).
 GN AGT1.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99103586; PubMed=9888511;
 RA Milligan D.S., Bird I.M.;
 RT "Isolation of an ovine genomic sequence containing the full-length
 angiotensin II type-1 receptor."
 RL Endocr. Res. 24:387-390(1998).
 RN [2]
 RP SEQUENCE OF 1-132 FROM N.A.
 RC TISSUE=Adrenal cortex;
 RX MEDLINE=98351904; PubMed=9687288;
 RA Bird I.M., Milligan D.S., Magness R.R.;
 RT "Specific pregnancy-induced angiotensin II type-1 receptor expression
 in ovine uterine artery does not involve formation of alternate splice
 variants or alternate promoter usage."
 RL Biol. Reprod. 59:219-224(1998).
 CC -1- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
 ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
 CALCIUM SECOND MESSENGER SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- PM: CARBOXY-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF069750; AAC99344.1; -
 DR EMBL: AF069750; AAC99344.1; -
 DR HSP: P34996; 1DD.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G-PROTEIN_RECP_FL_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
 KM Palmitate; Phosphorylation.
 FT DOMAIN 1 27
 FT TRANSMEM 28 52
 FT DOMAIN 53 64
 FT TRANSMEM 65 87
 FT DOMAIN 88 102
 FT TRANSMEM 103 124
 FT DOMAIN 125 142
 FT TRANSMEM 143 162
 FT DOMAIN 163 192
 FT TRANSMEM 193 214
 FT DOMAIN 215 240
 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 241 262 6 (POTENTIAL).
 FT DOMAIN 263 275 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 276 296 7 (POTENTIAL).
 FT DOMAIN 297 359 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFD 101 180 BY SIMILARITY.
 FT LIPID 355 355 PALMITATE (POTENTIAL).
 SQ SEQUENCE 359 AA; 41046 MW; C07010F1A110CE7 CRC64;

Query Match 100.0%; Score 52; DB 1; Length 359;
 Best Local Similarity 100.0%; Pctd. NO. 0.028;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGIRRIODD 10
 |||||||
 Db 8 EDGIRRIODD 17

RESULT 9
 AG2S_HUMAN STANDARD: PRT: 359 AA.
 ID AG2S_HUMAN STANDARD: PRT: 359 AA.
 AC 013725:
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Type-1B angiotensin II receptor (AT1B) (AT1BR).
 GN AGT1B OR AT2R1B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=94183213; PubMed=8135787;
 RA Konishi H., Kuroda S., Inada Y., Fujisawa Y.;
 RT "Novel subtype of human angiotensin II type 1 receptor: cDNA cloning
 and expression."
 RL Blochem. Biophys. Res. Commun. 199:467-474(1994).
 CC -1- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
 ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
 CALCIUM SECOND MESSENGER SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE LUNG, PLACENTA AND LIVER.
 CC -1- PM: CARBOXY-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: D13814; BAA02968.1; -
 DR HSP: P34996; 1DD.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G-PROTEIN_RECP_FL_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
 KM Palmitate; Phosphorylation.
 FT DOMAIN 1 27
 FT TRANSMEM 28 52
 FT DOMAIN 53 64
 FT TRANSMEM 65 87
 FT DOMAIN 88 102
 FT TRANSMEM 103 124
 FT DOMAIN 125 142
 CYTOPLASMIC (POTENTIAL).

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FT TRANSMEM 143 162 4 (POTENTIAL).
FT DOMAIN 163 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 214 5 (POTENTIAL).
FT DOMAIN 215 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 241 262 6 (POTENTIAL).
FT TRANSMEM 263 275 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 296 7 (POTENTIAL).
FT DOMAIN 297 359 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 101 180 BY SIMILARITY.
FT LIPID 355 355 PALMITATE (POTENTIAL).
SQ SEQUENCE 359 AA; 41020 MW; 298DFD3FF50D4EA4 CRC64;

Query Match 100.0%; Score 52; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EDGIRRIODD 10
Db 8 EDGIRRIODD 17

RESULT 10
AG2S_MOUSE STANDARD: PRT: 359 AA.
ID AG2S_MOUSE
AC P29755;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Type-1B angiotensin II receptor (AT1B) (AT3).
GN AGR1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-Liver;
RX MEDLINE=92287102; PubMed=1599461;
RA Sasamura H., Hein L., Krieger J.E., Pratt R.E., Koblika B.K.,
RA Dzeu V.J.;
RT "Cloning, characterization, and expression of two angiotensin
RT receptor (AT-1) isoforms from the mouse genome.";
RL Biochem. Biophys. Res. Commun. 185:253-259(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92359981; PubMed=1497638;
RA Yoshida H., Kakuchi J., Guo D.F., Furuta H., Iwai N.,
RA van der Meer-de Jong R., Inagami T., Ichikawa I.;
RT "Analysis of the evolution of angiotensin II type 1 receptor gene in
RT mammals (mouse, rat, bovine and human).";
RL Biochem. Biophys. Res. Commun. 186:1042-1049(1992).
CC -1- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC or send an email to license@sib-sib.ch).
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CC EMBL: S37491; AAB22270.1; .
CC PIR: JH0622; JH0622.
CC PIR: JC1194; JC1194.
CC HSSP: P34996; IDDD.

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DR MGD: MGI:87965; Agt1b.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHOPOPSN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
KW Palmitate; Phosphorylation.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 52 1 (POTENTIAL).
FT DOMAIN 53 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 87 2 (POTENTIAL).
FT DOMAIN 88 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT TRANSMEM 125 142 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 143 162 4 (POTENTIAL).
FT TRANSMEM 163 192 5 (POTENTIAL).
FT TRANSMEM 193 214 6 (POTENTIAL).
FT TRANSMEM 215 240 7 (POTENTIAL).
FT TRANSMEM 241 262 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 263 275 7 (POTENTIAL).
FT TRANSMEM 276 296 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 297 359 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 101 180 BY SIMILARITY.
FT LIPID 355 355 PALMITATE (POTENTIAL).
FT CONFLICT 7 7 I -> T (IN REF. 2).
FT CONFLICT 166 166 H -> Y (IN REF. 2).
FT CONFLICT 173 173 E -> A (IN REF. 2).
FT CONFLICT 205 205 V -> E (IN REF. 2).
FT CONFLICT 232 232 T -> I (IN REF. 2).
FT CONFLICT 239 239 F -> G (IN REF. 2).
SQ SEQUENCE 359 AA; 40949 MW; 95730F97058BAAB CRC64;

Query Match 100.0%; Score 52; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EDGIRRIODD 10
Db 8 EDGIRRIODD 17

RESULT 11
AG2S_RAT STANDARD: PRT: 359 AA.
ID AG2S_RAT
AC P29089;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Type-1B angiotensin II receptor (AT1B) (AT3).
GN AGR1B OR AT1B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley;
RX MEDLINE=92183879; PubMed=1544458;
RA Iwai N., Inagami T.;
RT "Identification of two subtypes in the rat type I angiotensin II
RT receptor.";
RL FEBS Lett. 298:257-260(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Adrenal cortex;
RX MEDLINE=92250585; PubMed=1374402;
RA Sandberg K., Ji H., Clark A.J., Shapira H., Gatt K.J.;
RT "Cloning and expression of a novel angiotensin II receptor subtype.";
RL J. Biol. Chem. 267:9455-9458(1992).

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[3]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Anterior pituitary;
 RX MEDLINE=92231868; PubMed=1567388;
 RA Kakar S.S., Sellers J.C., Devor D.C., Musgrove L.C., Neill J.D.;
 RT "Angiotensin II type-1 receptor subtype cDNAs: differential tissue
 RL expression and hormonal regulation."
 RL Biochem. Biophys. Res. Commun. 183:1090-1096(1992).
 RN [4]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=92246922; PubMed=1575725;
 RA Elton T.S., Stephan C.C., Taylor G.R., Kimball M.G., Martin M.M.,
 RA Durand J.N., Opatil S.;
 RT "Isolation of two distinct type I angiotensin II receptor genes."
 RL Biochem. Biophys. Res. Commun. 184:1067-1073(1992).
 CC -1- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
 CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
 CC CALCIUM SECOND MESSENGER SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: IS EXPRESSED IN THE LIVER, KIDNEY, AORTA,
 CC LUNG, UTERUS, OVARY, SPLEEN, HEART, ADRENAL GLAND, AND VASCULAR
 CC SMOOTH MUSCLE CELL.
 CC -1- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO FAMILY I OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 CC DR EMBL: X64052; CAA45410.1; -;
 CC DR EMBL: M90065; AAA40704.1; -;
 CC DR EMBL: M87003; AAA40739.1; -;
 CC DR PIR: A42656; A42656.
 CC DR PIR: S20423; S20423.
 CC DR PIR: JH0578; JH0578.
 CC DR PIR: J01516; J01516.
 CC DR HSSP: P34996; 1DDO.
 CC DR InterPro: IPR000276; GPCR_Rhodopsn.
 CC DR Pfam: PF00001; 7tm1.1; 1
 CC PRINTS: PR00237; GPCR_Rhodopsn.
 CC DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1; 1.
 CC DR PROSITE: PS50262; G-PROTEIN_RECP_F1_2; 1.
 CC KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Phosphorylation.
 CC -----
 CC FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 28 52 1 (POTENTIAL).
 CC FT DOMAIN 53 64 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 65 87 2 (POTENTIAL).
 CC FT DOMAIN 88 102 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 103 124 3 (POTENTIAL).
 CC FT DOMAIN 125 142 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 143 162 4 (POTENTIAL).
 CC FT DOMAIN 163 192 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 193 214 5 (POTENTIAL).
 CC FT DOMAIN 215 240 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 241 262 6 (POTENTIAL).
 CC FT DOMAIN 263 275 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 276 296 7 (POTENTIAL).
 CC FT DOMAIN 297 359 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 359 400 4 (POTENTIAL).
 CC FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT DISULFID 101 180 BR SIMILARITY.
 CC FT CONFLICT 2 2 T -> I (IN REF. 3 AND 4).
 CC FT CONFLICT 40 40 L -> Y (IN REF. 3 AND 4).
 CC FT CONFLICT 75 75 L -> Y (IN REF. 4).
 CC FT SEQUENCE 359 AA; 40911 MW; A2CC21E0B365C5B CRC64;
 Query Match 100.0%; Score 52; DB 1; Length 359;

Best Local Similarity 100.0%; Pred. No. 0.028;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 EDGIRIIDD 10
 Db 8 EDGIRIIDD 17
 RESULT 12
 AG2R_MERUN
 ID AG2R_MERUN STANDARD: PRT: 359 AA.
 AC 035210.
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Type-1 angiotensin II receptor (AT1) (GKAT1).
 GN AGRI1.
 OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
 OC Meriones.
 OX NCBI_TaxID=10047;
 CC [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=98434644; PubMed=9757050;
 RA Moriuchi R., Shibata S., Himeno A., Johren O., Hoe K.L.,
 RA Saavedra J.M.;
 RT "Molecular cloning and pharmacological characterization of an atypical
 RT gerbil angiotensin II type-1 receptor and its mRNA expression in brain
 RT and peripheral tissues."
 RL Brain Res. Mol. Brain Res. 60:234-246(1998).
 CC -1- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
 CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
 CC CALCIUM SECOND MESSENGER SYSTEM (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO FAMILY I OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 CC DR EMBL: AF011903; AAB65429.1; -;
 CC DR HSSP: P34996; 1DDO.
 CC DR InterPro: IPR000276; GPCR_Rhodopsn.
 CC DR Pfam: PF00001; 7tm1.1; 1.
 CC PRINTS: PR00237; GPCR_Rhodopsn.
 CC DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1; 1.
 CC DR PROSITE: PS50262; G-PROTEIN_RECP_F1_2; 1.
 CC KW G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
 CC Palmitate; Phosphorylation.
 CC -----
 CC FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 28 52 1 (POTENTIAL).
 CC FT DOMAIN 53 64 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 65 87 2 (POTENTIAL).
 CC FT DOMAIN 88 102 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 103 124 3 (POTENTIAL).
 CC FT DOMAIN 125 142 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 143 162 4 (POTENTIAL).
 CC FT DOMAIN 163 192 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 193 214 5 (POTENTIAL).
 CC FT DOMAIN 215 240 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 241 262 6 (POTENTIAL).
 CC FT DOMAIN 263 275 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 276 296 7 (POTENTIAL).
 CC FT DOMAIN 297 359 CYTOPLASMIC (POTENTIAL).
 CC FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 188 188

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FT DISULFID 101 180 BY SIMILARITY.
FT LIPID 355 355 PALMITATE (POTENTIAL).
SQ SEQUENCE 359 AA; 40779 MW; 84C1E9B9C64736DD CRC64;

Query Match
Best Local Similarity 90.0%; Score 49; DB 1; Length 359;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGIRRIODD 10
Db 8 DDGIRRIODD 17

RESULT 13
AG2R_PIG STANDARD; PRT; 359 AA.
AC P30555;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Type-1 angiotensin II receptor (AT1).
GN AGRI.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
ON NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Aortic smooth muscle;
RX MEDLINE=9325923; PubMed=8491254;
RA Itazaki K., Shigeri Y., Fujimoto M.;
RT "Molecular cloning and characterization of the angiotensin receptor
RT subtype in porcine aortic smooth muscle.";
RL Eur. J. Pharmacol. 245:147-156(1993).
CC -1- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- PM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; D1340; BAA01952.1; -
DR HSSP; P34996; 1DD.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G-PROTEIN_RECPE_FL_1; 1.
DR PROSITE; PS50262; G-PROTEIN_RECPE_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
KW Palmitate; Phosphorylation.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 52 1 (POTENTIAL).
FT DOMAIN 53 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 87 2 (POTENTIAL).
FT DOMAIN 88 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT TRANSMEM 125 142 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 143 162 4 (POTENTIAL).
FT DOMAIN 163 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 214 5 (POTENTIAL).
FT DOMAIN 215 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 241 262 6 (POTENTIAL).
FT DOMAIN 263 275 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 296 7 (POTENTIAL).
FT DOMAIN 297 359 CYTOPLASMIC (POTENTIAL).

```

```

FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 101 180 BY SIMILARITY.
FT LIPID 355 355 PALMITATE (POTENTIAL).
SQ SEQUENCE 359 AA; 40906 MW; D5B93968CC57ABF0 CRC64;

Query Match
Best Local Similarity 88.5%; Score 46; DB 1; Length 359;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDGIRRIODD 10
Db 8 EDSIRRIODD 17

RESULT 14
FABG_BUCAL STANDARD; PRT; 244 AA.
AC P57432;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
DE acyl carrier protein reductase).
GN FABG OR BU351.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
ON NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tokyo 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
CC PATHWAY.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SCR) FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AP001119; BAB13055.1; -
DR HSSP; P25529; IFMC.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
DR Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
KW NP_BIND 10 34 NADP (BY SIMILARITY).
FT ACT_SITE 151 151 BY SIMILARITY.
SQ SEQUENCE 244 AA; 26894 MW; A6A9AC8ACEACE66 CRC64;

Query Match
Best Local Similarity 76.9%; Score 40; DB 1; Length 244;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDGIRRIOD 9
Db 39 EDGVRIND 47

```

```

RESULT 15
NH16_CAEEL STANDARD: PRT: 388 AA.
ID NH16_CAEEL
AC Q27521: Q9XVB9;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nuclear hormone receptor family member nhr-16.
GN NHR-16 OR T12C9.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99148134; PubMed=10022975;
RA Sluder A.E., Mathews S.W., Hough D., Yin V.P., Malna C.V.;
RT "The nuclear receptor superfamily has undergone extensive
RT proliferation and diversification in nematodes."
RL Genome Res. 9:103-120(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RA Pauley A.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP REVISIONS.
RA Waterston R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ORPHAN NUCLEAR RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF083231; AAD03689.1; -.
DR EMBL: U41104; AAK67239.1; -.
DR HSSP: P20393; 1A6Y.
DR WormPep: T12C9.1; CE04933.
DR InterPro: IPR000536; Hormone_rec_1lg.
DR InterPro: IPR001628; Znf_C4steroid.
DR Pfam: PF00104; hormone_rec_1.
DR Pfam: PF00105; zf-C4_1.
DR PRINTS: PR00047; STROIDFINGER.
DR ProDom: PD000035; Znf_C4steroid; 1.
DR SMART: SM00430; HOLY.1.
DR SMART: SM00399; Znf_C4_1.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
DR Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger.
FT DNA_BIND 14 79 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 14 34 C4-TYPE.
FT ZN_FING 50 74 C4-TYPE.
SQ SEQUENCE 388 AA; 44462 MW; 2F0F0A56B4793EB3 CRC64;

Query Match 73.1%; Score 38; DB 1; Length 388;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
OY 1 EDGIRKRIQDD 10
DB 355 QKGVRRIQDD 364

```

Search completed: November 12, 2002, 16:16:48
Job time : 11 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:15:53 ; Search time 35 Seconds
(without alignments)
38.072 Million cell updates/sec

Title: US-09-540-816-1
Perfect score: 52
Sequence: 1 EDGIKRIQDD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 segs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SID2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SID2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SID2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SID2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SID2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SID2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SID2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SID2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SID2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SID2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SID2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SID2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SID2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SID2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SID2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	10	AA72230	Epitope of rat vas
2	52	100.0	15	AA74531	Human angiotensin
3	52	100.0	359	AA802844	Human G protein co
4	52	100.0	359	AA802848	Human G protein co
5	52	100.0	359	AA802849	Human G protein co
6	52	100.0	359	AA802850	Human G protein co
7	52	100.0	359	AA802851	Human G protein co
8	52	100.0	359	AA802854	Human Angiotensin
9	52	100.0	359	AA802855	Human Angiotensin
10	52	100.0	359	AA802856	Human Angiotensin

11	52	100.0	360	21	AA802851
12	44	84.6	228	21	AA814361
13	44	84.6	225	21	AA814360
14	44	84.6	302	21	AA814359
15	40	76.9	321	21	AA844213
16	40	76.9	321	21	AA844214
17	40	76.9	322	21	AA844212
18	40	76.9	322	21	AA844211
19	40	76.9	361	21	AA844211
20	40	76.9	361	21	AA844211
21	39	75.0	13	15	AA867111
22	37	71.2	367	22	AA866832
23	37	71.2	403	22	AA858218
24	36	69.2	193	21	AA847973
25	36	69.2	260	22	AA880086
26	36	69.2	342	23	AA847463
27	36	69.2	370	22	AA847623
28	36	69.2	417	20	AA806206
29	36	69.2	421	22	AA892608
30	36	69.2	421	22	AA880084
31	36	69.2	440	19	AA826782
32	36	69.2	442	22	AA865401
33	36	69.2	465	22	AA896333
34	36	69.2	563	22	AA870714
35	36	69.2	1083	22	AA879921
36	36	69.2	1151	22	AA878937
37	35	67.3	71	22	AA833430
38	35	67.3	75	22	AA835325
39	35	67.3	91	22	AA859444
40	35	67.3	352	21	AA853423
41	35	67.3	455	15	AA846606
42	35	67.3	487	22	AA873911
43	35	67.3	1193	22	AA825602
44	35	67.3	1193	23	AA861824
45	35	67.3	1194	22	AA832407

ALIGNMENTS

RESULT 1
AA72230
ID AA72230 standard; Peptide: 10 AA.
XX
AC AA72230;
DT 01-DEC-1995 (first entry)
XX
DE
XX
KW Monoclonal antibody; AT1 receptor; subtype; Angiotensin II receptor;
KW rat vascular smooth muscle; conserved; mammalian AT1 receptor;
KW detection; cancer diagnosis; sperm motility; contraception.
XX
OS Synthetic.
OS
PN [MO9509186-A]
PD 06-APR-1995.
XX
PF 27-SEP-1994; 94WO-GB02100.
XX
PR 27-SEP-1993; 93GB-0019877.
XX
PA (QUEB-) QUEBEN MARY & WESTFIELD COLLEGE.
XX
PI Barker S, Vinson GP;
XX
DR WPI; 1995-147395/19.
XX
PT Monoclonal antibody to AT1 angiotensin receptor - used for
PT detection and control of uterine contractions and
PT vasoconstriction e.g. for treating hypertension

```
XX Claim 3; Page 13; 24pp; English.
PS
XX
CC Monoclonal antibodies (MABs) that bind to the AT1 receptor (a
CC subtype of Angiotensin II receptor) are claimed. The Abs
CC specifically bind to amino acid residues 8 to 17 of the rat vascular
CC smooth muscle AT1 receptor. This sequence is conserved in all
CC mammalian AT1 receptors so far cloned. The Mabs can be used for
CC detection of AT1 receptors, e.g. in cancer diagnosis. They can also
CC be used to study and measure sperm motility and can be used in
CC contraception.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 52; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGIRRIQDD 10
   |||||
Db 1 EDGIRRIQDD 10

RESULT 2
AAR44531
ID AAR44531 standard; Protein; 359 AA.
XX
AC AAR44531;
XX
DT 24-JUN-1994 (first entry)
XX
DE Human angiotensin II type 1 receptor.
XX
KW Angiotensin; Ang II; receptor; antagonist; hypertension.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 187..313
   /note="claim 1"
XX
PM CA2093495-A.
XX
PD 08-OCT-1993.
XX
PF 06-APR-1993; 93CA-2093495.
XX
PR 07-APR-1992; 92JP-0085445.
PR 21-APR-1992; 92JP-0101393.
PR 17-FEB-1993; 93JP-0027835.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Fujisawa Y, Konishi H, Kuroda S;
XX
DR WPI; 1994-000128/01.
DR N-PSDB; AA053486.
XX
PT Human angiotensin II type 1 receptor polypeptide - useful for
PT determining human angiotensin II type 1 receptor antagonist
PT activity
XX
PS Claim 2; Fig 1; 42pp; English.
XX
CC Human Ang II type 1 receptor is useful for determining the
CC bioactivity of angiotensin II type 1 receptor antagonists which are
CC useful for treating hypertension. The Ang II type 1 receptor gene
CC was derived from human placenta and is contained in plasmid
CC PHARpl16.
XX
SQ Sequence 359 AA;

Query Match 100.0%; Score 52; DB 15; Length 359;
```

```
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGIRRIQDD 10
   |||||
Db 8 EDGIRRIQDD 17

RESULT 3
AAB02844
ID AAB02844 standard; Protein; 359 AA.
XX
AC AAB02844;
XX
DT 22-AUG-2000 (first entry)
XX
DE Human G protein coupled receptor AT1 protein SEQ ID NO:66.
XX
KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
KW identification; agonist; screening; therapeutic; pharmaceutical;
KW mutant.
XX
OS Homo sapiens.
XX
PN WO200022131-A2.
XX
PD 20-APR-2000.
XX
PF 13-OCT-1999; 99WO-US24065.
XX
PR 13-OCT-1998; 98US-0170496.
PR 12-NOV-1998; 98US-0108029.
PR 20-NOV-1998; 98US-0109213.
PR 27-NOV-1998; 98US-0110060.
PR 16-FEB-1999; 99US-0120416.
PR 26-FEB-1999; 99US-0121852.
PR 12-MAR-1999; 99US-0123944.
PR 12-MAR-1999; 99US-0123945.
PR 12-MAR-1999; 99US-0123946.
PR 12-MAR-1999; 99US-0123948.
PR 12-MAR-1999; 99US-0123949.
PR 12-MAR-1999; 99US-0123951.
PR 28-MAY-1999; 99US-0136436.
PR 28-MAY-1999; 99US-0136437.
PR 28-MAY-1999; 99US-0136439.
PR 28-MAY-1999; 99US-0137127.
PR 28-MAY-1999; 99US-0137131.
PR 28-MAY-1999; 99US-0137567.
PR 30-JUN-1999; 99US-0141448.
PR 27-JUN-1999; 99US-0151114.
PR 03-SEP-1999; 99US-0152524.
PR 29-SEP-1999; 99US-0156633.
PR 29-SEP-1999; 99US-0156555.
PR 29-SEP-1999; 99US-0156634.
XX
XX (AREN-) ARENA PHARM INC.
XX
PI Behan DP, Lehmann-Brunisma K, Chalmers DT, Chen R, Dang HT;
PI Gore M, Liaw CW, Lin Y, Lowitz K, White C;
XX
DR WPI; 2000-317986/27.
DR N-PSDB; AAA46062.
XX
PT Non-endogenous, human G protein-coupled receptors for screening
PT receptor, inverse or partial agonists useful as therapeutic agents -
XX
PS Example 1; Page 129-130; 187pp; English.
XX
CC The present invention describes transmembrane receptors, preferably
CC human G protein coupled receptors (GPCR), for which the endogenous
CC ligand is unknown (orphan GPCR receptors). More specifically the present
CC invention relates to non-endogenous, constitutively activated versions
CC of a human GPCR. These non-endogenous human GPCRs can be useful for
```


CC the direct identification of candidate compounds as receptors agonists,
CC inverse agonists or partial agonists for use as pharmaceutical agents.
CC AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
CC the exemplification of the present invention.

XX SQ Sequence 359 AA;

Query Match 100.0%; Score 52; DB 21; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGKRIODD 10
|||||
DB 8 EDGKRIODD 17

RESULT 4
AAB02848
ID AAB02848 standard; Protein; 359 AA.

XX AC AAB02848;

XX DT 22-AUG-2000 (first entry)

XX DE Human G protein coupled receptor hAT1 F239K protein SEQ ID NO:90.

XX KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
XX identification; agonist; screening; therapeutic; pharmaceutical;
XX mutant.

OS Homo sapiens.

OS Synthetic.

XX PN WO200022131-A2.

XX PD 20-APR-2000.

XX PF 13-OCT-1999; 99WO-US24065.

XX PR 13-OCT-1998; 98US-0170496.

XX PR 12-NOV-1998; 98US-0108029.

XX PR 20-NOV-1998; 98US-0109213.

XX PR 27-NOV-1998; 98US-0110060.

XX PR 16-FEB-1999; 99US-0120416.

XX PR 26-FEB-1999; 99US-0121852.

XX PR 12-MAR-1999; 99US-0123944.

XX PR 12-MAR-1999; 99US-0123945.

XX PR 12-MAR-1999; 99US-0123946.

XX PR 12-MAR-1999; 99US-0123948.

XX PR 12-MAR-1999; 99US-0123949.

XX PR 12-MAR-1999; 99US-0123949.

XX PR 28-MAY-1999; 99US-0136436.

XX PR 28-MAY-1999; 99US-0136437.

XX PR 28-MAY-1999; 99US-0136439.

XX PR 28-MAY-1999; 99US-0137127.

XX PR 28-MAY-1999; 99US-0137131.

XX PR 28-MAY-1999; 99US-0137567.

XX PR 30-JUN-1999; 99US-0141448.

XX PR 27-AUG-1999; 99US-0151114.

XX PR 03-SEP-1999; 99US-0152524.

XX PR 29-SEP-1999; 99US-0156633.

XX PR 29-SEP-1999; 99US-0156555.

XX PR 29-SEP-1999; 99US-0156634.

XX PA (AREN-) ARENA PHARM INC.

XX PI Behan DP, Iejmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;

XX PI Gore M, Iiaw CW, Lin I, Lowitz K, White C;

XX DR MPI: 2000-317986/27.

XX DR N-PSDB; AAA46082.

XX PT Non-endogenous, human G protein-coupled receptors for screening

PT receptor, inverse or partial agonists useful as therapeutic agents
XX
XX Example 2; Page 143-144; 187pp; English.

CC The present invention describes transmembrane receptors, preferably
CC human G protein coupled receptors (GPCR), for which the endogenous
CC ligand is unknown (orphan GPCR receptors). More specifically the present
CC invention relates to non-endogenous, constitutively activated versions
CC of a human GPCR. These non-endogenous human GPCRs can be useful for
CC the direct identification of candidate compounds as receptors agonists,
CC inverse agonists or partial agonists for use as pharmaceutical agents.
CC AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
CC the exemplification of the present invention.

XX SQ Sequence 359 AA;

Query Match 100.0%; Score 52; DB 21; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGKRIODD 10
|||||
DB 8 EDGKRIODD 17

RESULT 5
AAB02849
ID AAB02849 standard; Protein; 359 AA.

XX AC AAB02849;

XX DT 22-AUG-2000 (first entry)

XX DE Human G protein coupled receptor hAT1 mutant protein SEQ ID NO:94.

XX KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
XX identification; agonist; screening; therapeutic; pharmaceutical;
XX mutant.

OS Homo sapiens.

OS Synthetic.

XX PN WO200022131-A2.

XX PD 20-APR-2000.

XX PF 13-OCT-1999; 99WO-US24065.

XX PR 13-OCT-1998; 98US-0170496.

XX PR 12-NOV-1998; 98US-0108029.

XX PR 20-NOV-1998; 98US-0109213.

XX PR 27-NOV-1998; 98US-0110060.

XX PR 16-FEB-1999; 99US-0120416.

XX PR 26-FEB-1999; 99US-0121852.

XX PR 12-MAR-1999; 99US-0123944.

XX PR 12-MAR-1999; 99US-0123945.

XX PR 12-MAR-1999; 99US-0123946.

XX PR 12-MAR-1999; 99US-0123948.

XX PR 12-MAR-1999; 99US-0123949.

XX PR 12-MAR-1999; 99US-0123951.

XX PR 28-MAY-1999; 99US-0136436.

XX PR 28-MAY-1999; 99US-0136437.

XX PR 28-MAY-1999; 99US-0137127.

XX PR 28-MAY-1999; 99US-0137131.

XX PR 28-MAY-1999; 99US-0137567.

XX PR 30-JUN-1999; 99US-0141448.

XX PR 27-AUG-1999; 99US-0151114.

XX PR 03-SEP-1999; 99US-0152524.

XX PR 29-SEP-1999; 99US-0156633.

XX PR 29-SEP-1999; 99US-0156555.

XX PR 29-SEP-1999; 99US-0156634.

PA (AREN-) ARENA PHARM INC.
 XX 28-MAY-1999; 99US-0137131.
 PI Behan DP, Lehmann-Brinisma K, Chalmers DT, Chen R, Dang HT;
 PI Gore M, Liaw CM, Lin I, Lowitz K, White C;
 XX WPI: 2000-317986/27.
 DR N-PSDB; AAA46084.
 XX
 PT Non-endogenous, human G protein-coupled receptors for screening
 PT receptor, inverse or partial agonists useful as therapeutic agents
 XX
 PS Example 2; Page 146-147; 187pp; English.
 CC The present invention describes transmembrane receptors, preferably
 CC human G protein coupled receptors (GPCR), for which the endogenous
 CC ligand is unknown (orphan GPCR receptors). More specifically the present
 CC invention relates to non-endogenous, constitutively activated versions
 CC of a human GPCR. These non-endogenous human GPCRs can be useful for
 CC the direct identification of candidate compounds as receptors agonists,
 CC inverse agonists or partial agonists for use as pharmaceutical agents.
 CC AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
 CC the exemplification of the present invention.
 CC
 XX Sequence 359 AA:
 SQ
 Query Match 100.0%; Score 52; DB 21; Length 359;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EDGIRIQQDD 10
 |||||
 DB 8 EDGIRIQQDD 17
 XX
 RESULT 6
 AAB02850
 ID AAB02850 standard; Protein; 359 AA.
 XX
 AC AAB02850;
 XX
 DT 22-AUG-2000 (first entry)
 XX
 DE Human G protein coupled receptor hAT1 mutant protein SEQ ID NO:100.
 XX
 KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
 KW identification; agonist; screening; therapeutic; pharmaceutical;
 KW mutant.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200022131-A2.
 XX
 PD 20-APR-2000.
 XX
 PF 13-OCT-1999; 99WO-US24065.
 XX
 PR 13-OCT-1998; 98US-0170496.
 PR 12-NOV-1998; 98US-0108029.
 PR 20-NOV-1998; 98US-0109213.
 PR 27-NOV-1998; 98US-0110060.
 PR 16-FEB-1999; 99US-0120416.
 PR 26-FEB-1999; 99US-0121852.
 PR 12-MAR-1999; 99US-0123944.
 PR 12-MAR-1999; 99US-0123945.
 PR 12-MAR-1999; 99US-0123946.
 PR 12-MAR-1999; 99US-0123948.
 PR 12-MAR-1999; 99US-0123949.
 PR 12-MAR-1999; 99US-0123951.
 PR 28-MAY-1999; 99US-0136436.
 PR 28-MAY-1999; 99US-0136437.
 PR 28-MAY-1999; 99US-0136439.
 PR 28-MAY-1999; 99US-0137127.

PR 28-MAY-1999; 99US-0137131.
 PR 28-MAY-1999; 99US-0137567.
 PR 30-JUN-1999; 99US-0141448.
 PR 27-AUG-1999; 99US-0151114.
 PR 03-SEP-1999; 99US-0152524.
 PR 29-SEP-1999; 99US-0156633.
 PR 29-SEP-1999; 99US-0156555.
 PR 29-SEP-1999; 99US-0156634.
 XX
 PA (AREN-) ARENA PHARM INC.
 XX
 PI Behan DP, Lehmann-Brinisma K, Chalmers DT, Chen R, Dang HT;
 PI Gore M, Liaw CM, Lin I, Lowitz K, White C;
 XX WPI: 2000-317986/27.
 DR N-PSDB; AAA46090.
 XX
 PT Non-endogenous, human G protein-coupled receptors for screening
 PT receptor, inverse or partial agonists useful as therapeutic agents
 XX
 PS Example 2; Page 150-151; 187pp; English.
 CC The present invention describes transmembrane receptors, preferably
 CC human G protein coupled receptors (GPCR), for which the endogenous
 CC ligand is unknown (orphan GPCR receptors). More specifically the present
 CC invention relates to non-endogenous, constitutively activated versions
 CC of a human GPCR. These non-endogenous human GPCRs can be useful for
 CC the direct identification of candidate compounds as receptors agonists,
 CC inverse agonists or partial agonists for use as pharmaceutical agents.
 CC AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
 CC the exemplification of the present invention.
 CC
 XX Sequence 359 AA:
 SQ
 Query Match 100.0%; Score 52; DB 21; Length 359;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EDGIRIQQDD 10
 |||||
 DB 8 EDGIRIQQDD 17
 XX
 RESULT 7
 AAO20951
 ID AAO20951 standard; Protein; 359 AA.
 XX
 AC AAO20951;
 XX
 DT 11-JUL-2002 (first entry)
 XX
 DE Protein of the angiotensin II type 1 (AT-1) receptor.
 XX
 KW Cardiovascular; vasotropic; angiotensin II; aortic valve disease;
 KW angiotensin converting enzyme; aortic valve; aortic stenosis; ACE;
 KW inhibiting agent; angiotensin II type 1 receptor antagonist;
 KW aortic sclerosis; AT-1.
 XX
 OS Homo sapiens.
 OS
 PN WO200228421-A1.
 XX
 PD 11-APR-2002.
 XX
 PF 05-OCT-2001; 2001WO-US31605.
 PF 06-OCT-2000; 2000US-238367P.
 PR
 XX (UNITW) UNIV WASHINGTON.
 PA
 PI O'Brien KD, Otto CM, Probstfield JJ,
 XX WPI: 2002-372197/40.

DR N-PSDB; AAK99740.
 XX Decreasing the amount and/or biological activity of angiotensin II in
 PT an aortic valve comprises administering angiotensin II inhibiting agent
 PT consisting of antagonists of angiotensin converting enzyme and the
 PT angiotensin II type I receptor
 XX
 PS Disclosure: Page 36-37; 40pp; English.
 XX
 CC The invention relates to a method for decreasing the amount and/or
 CC biological activity of angiotensin II in an aortic valve in an animal.
 CC This method comprises administering an angiotensin II inhibiting agent
 CC consisting of angiotensin converting enzyme (ACE) antagonists and
 CC angiotensin II type I receptor antagonists. The method is also useful to
 CC prevent progression and/or complications of aortic valve disease, such as
 CC aortic stenosis or aortic sclerosis. This sequence represents the protein
 CC of the angiotensin II type I (AT-1) receptor of the invention.
 XX
 SQ Sequence 359 AA:
 Query Match 100.0%; Score 52; DB 23; Length 359;
 Best Local Similarity 100.0%; Pred. No. 0.13; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EDGIRKIQDD 10
 Db 8 EDGIRKIQDD 17
 RESULT 8
 AAU78654
 ID AAU78654 standard; Protein; 359 AA.
 AC AAU78654;
 XX
 XX 18-JUN-2002 (first entry)
 DT
 XX
 DE Human Angiotensin receptor 1, AGTRL.
 XX
 KW Human; angiotensin; receptor; AGTRL; hypotensive; hypertension;
 KW chromosome 3q21-q25; haplotype; genotype; drug screening.
 XX
 OS Homo sapiens.
 OS
 PN EPI184456-A2.
 XX
 PD 06-MAR-2002.
 XX
 PF 12-JUN-2001; 2001EP-0114230.
 XX
 PR 28-AUG-2000; 2000US-228542P.
 PR 30-MAY-2001; 2001US-0867915.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 PA
 PI Anastasio AE, Koshy B, Finkel K, Lee HH;
 XX
 XX WPI: 2002-282840/33.
 DR N-PSDB; AAK47350, AAK47351.
 XX
 PT Novel genetic variants of Angiotensin Receptor 1 isogenes, useful for
 PT improving efficiency and reliability in drug development for treating
 PT diseases associated with AGTRL activity, e.g. hypertension
 XX
 PS Claim 30; Fig 3; 44pp; English.
 XX
 CC The invention relates to an isolated polynucleotide comprising a first
 CC nucleotide sequence which comprises a angiotensin receptor 1 (AGTRL)
 CC isogene selected from isogenes 1-8 and 10 given in the specification.
 CC Also included are methods of haplotyping/genotyping the AGTRL gene
 CC of an individual, predicting a haplotype pair of an individual,
 CC identifying an association between a trait and at least one haplotype or
 CC haplotype pair of AGTRL gene, oligonucleotides and primers for

CC detecting polymorphisms in the AGTRL gene, a recombinant non-human
 CC organism transformed or transfected with an AGTRL gene, where the
 CC organism expresses a AGTRL protein encoded by the AGTRL gene or the
 CC polymorphic variant sequence, the polymorphic variant proteins of AGTRL,
 CC an anti-AGTRL protein monoclonal antibody, a computer system for
 CC storing and analysing polymorphism data for the AGTRL gene and
 CC a genome anthology for AGTRL gene. The polypeptide is useful in screening
 CC for drugs targeting AGTRL that are useful for treating hypertension. The
 CC methods are useful for improving the efficiency and reliability of
 CC several steps in the discovery and development of drugs for treating
 CC diseases associated with AGTRL activity. The methods are also useful for
 CC screening compounds targeting AGTRL. The antibody is useful in
 CC diagnostic, prognostic and therapeutic methods. The AGTRL gene is useful
 CC in studying the expression and function of AGTRL, and in expressing AGTRL
 CC protein for use in screening for candidate drugs to treat diseases
 CC related to AGTRL activity. The AGTRL gene is also useful in studying the
 CC effect of the variation on the biological activity of AGTRL as well as on
 CC the binding affinity of candidate drugs targeting AGTRL for the treatment
 CC of hypertension. The recombinant organism is useful for studying the
 CC expression of AGTRL isogenes in vivo, for in vivo screening and testing
 CC of drugs targeted against AGTRL protein, and for testing the efficacy of
 CC therapeutic agents and compounds for treating hypertension in a
 CC biological system. The gene for AGTRL is located on chromosome
 CC 3q21-q25. The present sequence is the AGTRL protein sequence.
 XX
 SQ Sequence 359 AA:
 Query Match 100.0%; Score 52; DB 23; Length 359;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EDGIRKIQDD 10
 Db 8 EDGIRKIQDD 17
 RESULT 9
 AAU78655
 ID AAU78655 standard; Protein; 359 AA.
 AC AAU78655;
 XX
 XX 18-JUN-2002 (first entry)
 DT
 XX
 DE Human Angiotensin receptor 1, AGTRL, variant #1.
 XX
 KW Human; angiotensin; receptor; AGTRL; hypotensive; hypertension;
 KW chromosome 3q21-q25; haplotype; genotype; drug screening.
 XX
 OS Homo sapiens.
 OS
 PN EPI184456-A2.
 XX
 PD 06-MAR-2002.
 XX
 PF 12-JUN-2001; 2001EP-0114230.
 XX
 PR 28-AUG-2000; 2000US-228542P.
 PR 30-MAY-2001; 2001US-0867915.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 PA
 PI Anastasio AE, Koshy B, Finkel K, Lee HH;
 XX
 XX WPI: 2002-282840/33.
 DR
 XX
 PT Novel genetic variants of Angiotensin Receptor 1 isogenes, useful for
 PT improving efficiency and reliability in drug development for treating
 PT diseases associated with AGTRL activity, e.g. hypertension
 XX

XX Claim 30; Page -: 44pp; English.
PS The invention relates to an isolated polynucleotide comprising a first
XX nucleotide sequence which comprises a angiotensin receptor 1 (AGTRL)
CC isogene selected from isogenes 1-8 and 10 given in the specification.
CC Also included are methods of haplotyping/genotyping the AGTRL gene
CC of an individual, predicting a haplotype pair of an individual,
CC identifying an association between a trait and at least one haplotype or
CC haplotype pair of AGTRL gene, oligonucleotides and primers for
CC detecting polymorphisms in the AGTRL gene, a recombinant non-human
CC organism transformed or transfected with an AGTRL gene, where the
CC organism expresses a AGTRL protein encoded by the AGTRL gene or the
CC polymorphic variant sequence, the polymorphic variant proteins of AGTRL,
CC an anti-AGTRL protein monoclonal antibody, a computer system for
CC storing and analysing polymorphism data for the AGTRL gene and
CC a genome anthology for AGTRL gene. The polypeptide is useful in screening
CC for drugs targeting AGTRL that are useful for treating hypertension. The
CC methods are useful for improving the efficiency and reliability of
CC several steps in the discovery and development of drugs for treating
CC diseases associated with AGTRL activity. The methods are also useful for
CC screening compounds targeting AGTRL. The antibody is useful in
CC diagnostic, prognostic and therapeutic methods. The AGTRL gene is useful
CC in studying the expression and function of AGTRL, and in expressing AGTRL
CC protein for use in screening for candidate drugs to treat diseases
CC related to AGTRL activity. The AGTRL gene is also useful in studying the
CC effect of the variation on the biological activity of AGTRL as well as on
CC the binding affinity of candidate drugs targeting AGTRL for the treatment
CC of hypertension. The recombinant organism is useful for studying the
CC expression of AGTRL isogenes in vivo, for in vivo screening and testing of
CC drugs targeted against AGTRL protein, and for testing the efficacy of
CC therapeutic agents and compounds for treating hypertension in a
CC biological system. The gene for AGTRL is located on chromosome
CC 3q21-q25. The present sequence is AGTRL variant protein sequence.
CC Note: The present sequence is not shown in the specification but
CC was created by the indexer using the AGTRL sequence appearing as
CC AAU78654 and the information in figure 3.
XX
SQ Sequence 359 AA:
Query Match 100.0%; Score 52; DB 23; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.13; Mismatches 0; Gaps 0;
Matches 10; Conservative 0; Indels 0; Gaps 0;
QY 1 EDGIRRIODD 10
| | | | | | | | | |
DB 8 EDGIRRIODD 17
RESULT 10
AAU78656
ID AAU78656 standard; Protein: 359 AA.
XX
AC AAU78656;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human Angiotensin receptor 1, AGTRL, variant #2.
XX
KW Human; angiotensin; receptor; AGTRL; hypotensive; hypertension;
XX chromosome 3q21-q25; haplotype; genotype; drug screening.
XX
OS Homo sapiens.
XX
FT Key Location/Qualifiers
FT Misc-difference 336 /note= "Wild-type Thr substituted by Met"
XX
PN EP1184456-A2.
XX
PD 06-MAR-2002.
XX
PF 12-JUN-2001; 2001EP-0114230.

XX 28-AUG-2000; 2000US-228542P.
PR 30-MAY-2001; 2001US-0867915.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Anastasio AE, Koshy B, Finkel K, Lee HH;
XX WPI; 2002-282840/33.
DR
PT Novel genetic variants of Angiotensin Receptor 1 isogenes, useful for
PT improving efficiency and reliability in drug development for treating
PT diseases associated with AGTRL activity, e.g. hypertension
XX
PS Claim 30; Page -: 44pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising a first
CC nucleotide sequence which comprises a angiotensin receptor 1 (AGTRL)
CC isogene selected from isogenes 1-8 and 10 given in the specification.
CC Also included are methods of haplotyping/genotyping the AGTRL gene
CC of an individual, predicting a haplotype pair of an individual,
CC identifying an association between a trait and at least one haplotype or
CC haplotype pair of AGTRL gene, oligonucleotides and primers for
CC detecting polymorphisms in the AGTRL gene, a recombinant non-human
CC organism transformed or transfected with an AGTRL gene, where the
CC organism expresses a AGTRL protein encoded by the AGTRL gene or the
CC polymorphic variant sequence, the polymorphic variant proteins of AGTRL,
CC an anti-AGTRL protein monoclonal antibody, a computer system for
CC storing and analysing polymorphism data for the AGTRL gene and
CC a genome anthology for AGTRL gene. The polypeptide is useful in screening
CC for drugs targeting AGTRL that are useful for treating hypertension. The
CC methods are useful for improving the efficiency and reliability of
CC several steps in the discovery and development of drugs for treating
CC diseases associated with AGTRL activity. The methods are also useful for
CC screening compounds targeting AGTRL. The antibody is useful in
CC diagnostic, prognostic and therapeutic methods. The AGTRL gene is useful
CC in studying the expression and function of AGTRL, and in expressing AGTRL
CC protein for use in screening for candidate drugs to treat diseases
CC related to AGTRL activity. The AGTRL gene is also useful in studying the
CC effect of the variation on the biological activity of AGTRL as well as on
CC the binding affinity of candidate drugs targeting AGTRL for the treatment
CC of hypertension. The recombinant organism is useful for studying the
CC expression of AGTRL isogenes in vivo, for in vivo screening and testing of
CC drugs targeted against AGTRL protein, and for testing the efficacy of
CC therapeutic agents and compounds for treating hypertension in a
CC biological system. The gene for AGTRL is located on chromosome
CC 3q21-q25. The present sequence is AGTRL variant protein sequence.
CC Note: The present sequence is not shown in the specification but
CC was created by the indexer using the AGTRL sequence appearing as
CC AAU78654 and the information in figure 3.
XX
SQ Sequence 359 AA:
Query Match 100.0%; Score 52; DB 23; Length 359;
Best Local Similarity 100.0%; Pred. NO. 0.13; Mismatches 0; Gaps 0;
Matches 10; Conservative 0; Indels 0; Gaps 0;
QY 1 EDGIRRIODD 10
| | | | | | | | | |
DB 8 EDGIRRIODD 17
RESULT 11
AAB02851
ID AAB02851 standard; Protein: 360 AA.
XX
AC AAB02851;
XX
DT 22-AUG-2000 (first entry)
XX
DE Human G protein coupled receptor hArl mutant protein SEQ ID NO:106.
XX
KW Human; G protein coupled receptor; GPCR; transmembrane receptor;

KM	Identification; agonist; screening; therapeutic; pharmaceutical;
XX	mutant.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200022131-A2.
XX	
PD	20-APR-2000.
XX	
PF	13-OCT-1999; 99WO-US24065.
XX	
PR	13-OCT-1998; 98US-0170496.
PR	12-NOV-1998; 98US-0108029.
PR	20-NOV-1998; 98US-0109213.
PR	27-NOV-1998; 98US-0110060.
PR	16-FEB-1999; 99US-0120416.
PR	26-FEB-1999; 99US-0121852.
PR	12-MAR-1999; 99US-0123944.
PR	12-MAR-1999; 99US-0123945.
PR	12-MAR-1999; 99US-0123946.
PR	12-MAR-1999; 99US-0123948.
PR	12-MAR-1999; 99US-0123949.
PR	12-MAR-1999; 99US-0123951.
PR	28-MAY-1999; 99US-0136436.
PR	28-MAY-1999; 99US-0136437.
PR	28-MAY-1999; 99US-0136439.
PR	28-MAY-1999; 99US-0137127.
PR	28-MAY-1999; 99US-0137131.
PR	28-MAY-1999; 99US-0137567.
PR	30-JUN-1999; 99US-0141448.
PR	27-AUG-1999; 99US-0151114.
PR	03-SEP-1999; 99US-0152524.
PR	29-SEP-1999; 99US-0156633.
PR	29-SEP-1999; 99US-0156555.
PR	29-SEP-1999; 99US-0156634.
XX	
PA	(AREN-) ARENA PHARM INC.
XX	
PI	Behan DP, Lehmann-Brunisma K, Chalmers DF, Chen R, Dang HT;
PI	Gore M, Liaw CW, Lin I, Lowitz K, White C;
XX	
DR	WI: 2000-317986/27.
DR	N-PSDB; AAA46095.
XX	
PT	Non-endogenous, human G protein-coupled receptors for screening
PT	receptor, inverse or partial agonists useful as therapeutic agents
XX	
PS	Example 2; Page 153-155; 187pp; English.
XX	
CC	The present invention describes transmembrane receptors, preferably
CC	human G protein coupled receptors (GPCR), for which the endogenous
CC	ligand is unknown (orphan GPCR receptors). More specifically the present
CC	invention relates to non-endogenous, constitutively activated versions
CC	of a human GPCR. These non-endogenous human GPCRs can be useful for
CC	the direct identification of candidate compounds as receptors agonists,
CC	inverse agonists or partial agonists for use as pharmaceutical agents.
CC	AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
CC	the exemplification of the present invention.
XX	
SQ	Sequence 360 AA:
Query Match	100.0%; Score 52; DB 21; Length 360;
Best Local Similarity	100.0%; Pred. No. 0.13; Indels 0; Gaps 0
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	1 EDGIRIQQDD 10
DB	8 EDGIRIQQDD 17

ID	AA014361	standard; Protein; 225 AA.
XX		
AC	AA014361;	
XX		
DT	17-OCT-2000	(first entry)
XX		
DE	Arabidopsis thaliana	protein fragment SEQ ID NO: 14194.
XX		
KW	protein identification; signal transduction pathway; metabolic pathway; hydridisation assay; genetic mapping; gene expression control; promoter; termination sequence.	
XX		
OS	Arabidopsis thaliana.	
PN	EP1033405-A2.	
XX		
PD	06-SEP-2000.	
PF		
XX	25-FEB-2000;	2000EP-0301439.
PR	25-FEB-1999;	99US-0121825.
PR	05-MAR-1999;	99US-0123180.
PR	09-MAR-1999;	99US-0123548.
PR	23-MAR-1999;	99US-0125788.
PR	25-MAR-1999;	99US-0126264.
PR	29-MAR-1999;	99US-0126785.
PR	01-APR-1999;	99US-0127462.
PR	06-APR-1999;	99US-0128234.
PR	08-APR-1999;	99US-0128714.
PR	16-APR-1999;	99US-0129845.
PR	19-APR-1999;	99US-0130077.
PR	21-APR-1999;	99US-0130449.
PR	23-APR-1999;	99US-0130510.
PR	28-APR-1999;	99US-0130891.
PR	30-APR-1999;	99US-0131449.
PR	30-APR-1999;	99US-0132048.
PR	04-MAY-1999;	99US-0132407.
PR	05-MAY-1999;	99US-0132484.
PR	06-MAY-1999;	99US-0132485.
PR	06-MAY-1999;	99US-0132486.
PR	07-MAY-1999;	99US-0132487.
PR	11-MAY-1999;	99US-0132863.
PR	14-MAY-1999;	99US-0134218.
PR	14-MAY-1999;	99US-0134219.
PR	14-MAY-1999;	99US-0134221.
PR	14-MAY-1999;	99US-0134370.
PR	18-MAY-1999;	99US-0134768.
PR	19-MAY-1999;	99US-0134941.
PR	20-MAY-1999;	99US-0135124.
PR	21-MAY-1999;	99US-0135353.
PR	24-MAY-1999;	99US-0135629.
PR	25-MAY-1999;	99US-0136021.
PR	27-MAY-1999;	99US-0136392.
PR	28-MAY-1999;	99US-0136782.
PR	01-JUN-1999;	99US-0137222.
PR	03-JUN-1999;	99US-0137528.
PR	04-JUN-1999;	99US-0137502.
PR	07-JUN-1999;	99US-0137724.
PR	08-JUN-1999;	99US-0138094.
PR	10-JUN-1999;	99US-0138540.
PR	10-JUN-1999;	99US-0138847.
PR	14-JUN-1999;	99US-0139119.
PR	16-JUN-1999;	99US-0139452.
PR	16-JUN-1999;	99US-0139453.
PR	17-JUN-1999;	99US-0139454.
PR	18-JUN-1999;	99US-0139455.
PR	18-JUN-1999;	99US-0139456.
PR	18-JUN-1999;	99US-0139457.
PR	18-JUN-1999;	99US-0139458.
PR	18-JUN-1999;	99US-0139459.
PR	18-JUN-1999;	99US-0139460.

PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145216.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.

PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 13-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154479.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 84.6%; Score 44; DB 21; Length 225;
Best Local Similarity 80.0%; Pred. No. 2.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDGIRRIODD 10
Db 16 EDGIRRIODD 25

RESULT 13
AA614360
ID AA614360 standard; Protein: 228 AA.
XX AA614360;
AC
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 14193.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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XX 25-FEB-1999; 99US-0121825.
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PR 09-MAR-1999; 99US-0123548.
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PR 29-OCT-1999; 99US-0162142.

Query Match 84.6%; Score 44; DB 21; Length 228;
Best Local Similarity 80.0%; Pred. No. 2.4;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 19 EDGIMRLDP 28

RESULT 14

AAG14359
ID AAG14359 standard; Protein; 302 AA.

XX AAG14359;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 14192.

KW Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

XX termination sequence.

OS Arabidopsis thaliana.

PN EPI033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
PE 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 84.6%; Score 44; DB 21; Length 302;
Best Local Similarity 80.0%; Pred. No. 3.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDGIRI0DD 10
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Db 93 EDGIRL0DD 102

RESULT 15
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XX AAG44213;
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DT 18-OCT-2000 (first entry)
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XX Arabidopsis thaliana protein fragment SPQ ID NO: 55353.
DE
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
OS
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XX Epi1033405-A2.
PM
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PD 06-SEP-2000.
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XX 25-FEB-2000; 2000EP-0301439.
PF
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PR 29-MAR-1999; 99US-0126785.
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PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142390.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.

PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
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PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
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PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
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PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
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PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 23-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.

PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0158293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
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PR 14-OCT-1999; 99US-0159337.
PR 14-OCT-1999; 99US-0159637.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
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PR 21-OCT-1999; 99US-0160770.
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PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 76.98; Score 40; DB 21; Length 321;
Best Local Similarity 70.08; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db 49 DDEILRLDD 58

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Job time : 36 secs

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OM protein - protein search, using sw model

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19.615 Million cell updates/sec

Title: US-09-540-816-1

Perfect score: 10

Sequence: 1 EDGIKRIODD 10

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	100.0	10	3	US-08-624-374-1
2	10	100.0	358	2	US-08-458-970A-11
3	10	100.0	359	1	US-08-041-219A-6
4	10	100.0	359	1	US-08-148-209A-4
5	10	100.0	359	1	US-08-417-122-6
6	7	70.0	13	2	US-08-934-222-104
7	7	70.0	13	2	US-08-933-402-104
8	7	70.0	13	2	US-09-207-621-104
9	7	70.0	13	2	US-08-532-818-104
10	7	70.0	13	3	US-09-231-797-104
11	7	70.0	13	3	US-08-934-224-104
12	7	70.0	13	3	US-08-933-843-104
13	7	70.0	13	4	US-09-413-492-104
14	5	50.0	11	4	US-09-410-025-10
15	5	50.0	25	4	US-09-019-346A-1
16	5	50.0	79	3	US-08-596-684F-6
17	5	50.0	102	3	US-08-946-329A-102
18	5	50.0	143	3	US-08-946-329A-52
19	5	50.0	181	3	US-08-848-580-12
20	5	50.0	220	1	US-08-588-163-3
21	5	50.0	220	1	US-09-111-070-3
22	5	50.0	247	4	US-08-858-207A-300
23	5	50.0	257	3	US-08-596-684F-7
24	5	50.0	332	3	US-09-320-878-16
25	5	50.0	377	2	US-08-969-106-6
26	5	50.0	377	4	US-09-054-492B-1
27	5	50.0	377	4	US-09-054-492B-1

28	5	50.0	380	4	US-09-134-001C-3830	Sequence 3830, Ap
29	5	50.0	381	2	US-09-193-877-2	Sequence 2, Appl
30	5	50.0	402	2	US-08-403-852D-19	Sequence 19, Appl
31	5	50.0	402	3	US-08-510-646B-20	Sequence 20, Appl
32	5	50.0	402	4	US-09-231-818-19	Sequence 19, Appl
33	5	50.0	407	4	US-08-955-957A-2	Sequence 2, Appl
34	5	50.0	410	2	US-08-449-986-2	Sequence 2, Appl
35	5	50.0	410	2	US-08-756-855-2	Sequence 4, Appl
36	5	50.0	416	4	US-08-965-048-4	Sequence 4, Appl
37	5	50.0	432	2	US-08-896-005-4	Sequence 5, Appl
38	5	50.0	432	2	US-08-896-005-5	Sequence 5, Appl
39	5	50.0	432	3	US-09-075-087-2	Sequence 2, Appl
40	5	50.0	432	4	US-09-472-971-1	Sequence 1, Appl
41	5	50.0	432	4	US-09-347-878-1	Sequence 1, Appl
42	5	50.0	448	2	US-08-884-072-1	Sequence 1, Appl
43	5	50.0	448	4	US-09-212-168-1	Sequence 1, Appl
44	5	50.0	451	1	US-08-417-330A-12	Sequence 12, Appl
45	5	50.0	471	2	US-08-477-451-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-624-374-1
; Sequence 1, Application US/08624374
; Patent No. 6063620
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: NOVEL HYBRIDOMA & MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES PRODUCED THEREBY
; NUMBER OF SEQUENCES: 1
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; MEDIUM TYPE: storable
; COMPUTER: Compaq Prolinea 5100e
; OPERATING SYSTEM: DOS 6.2/Windows 3.1
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/624,374
; FILING DATE: March 27, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB94/02100
; FILING DATE: 27-SEPT-1994
; APPLICATION NUMBER: GB 9319877.8
; FILING DATE: 27-SEPT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Klein, Richard M.
; REGISTRATION NUMBER: 33,000
; REFERENCE/DOCKET NUMBER: BKY 2 040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (216) 861-5582
; TELEFAX: (216) 241-1666
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; CELL LINE: Hybridoma
; US-08-624-374-1

Query Match 100.0%; Score 10; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGIKRIODD 10
DB 1 EDGIKRIODD 10

RESULT 2
US-08-458-970A-11
; Sequence 11, Application US/08458970A
; Patent No. 5861272
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: C5a Receptor
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,970A
; FILING DATE: June 2, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09234
; FILING DATE: 16 AUG 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-458-970A-11
; Query Match 100.0%; Score 10; DB 2; Length 358;
; Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EDGIRRIODD 10
Db 7 EDGIRRIODD 16
RESULT 3
US-08-041-219A-6
; Sequence 6, Application US/08041219A
; Patent No. 5427922
; GENERAL INFORMATION:
; APPLICANT: FUJISAWA, Yukio
; APPLICANT: KURODA, Shun-ichi
; APPLICANT: KONISHI, Hiroyuki
; TITLE OF INVENTION: ANGIOTENSIN II TYPE-1 RECEPTOR AND ITS
; TITLE OF INVENTION: PRODUCTION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WESNER, CANTOR, MUELLER & PLAYER
; STREET: 1233 20th Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/041,219A
; FILING DATE: 31-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 085445-1992
; FILING DATE: 07-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 101393-1992
; FILING DATE: 21-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 027635-1993
; FILING DATE: 17-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Douglas P.
; REGISTRATION NUMBER: 30,300
; REFERENCE/DOCKET NUMBER: P-8700-23781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-0400
; TELEFAX: (202) 835-0605
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: Placental
; US-08-041-219A-6
; Query Match 100.0%; Score 10; DB 1; Length 359;
; Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 8 EDGIRRIODD 17
RESULT 4
US-08-148-209A-4
; Sequence 4, Application US/08148209A
; Patent No. 5556780
; GENERAL INFORMATION:
; APPLICANT: Dzau, Victor J
; APPLICANT: Muroyama, Masashi
; TITLE OF INVENTION: TYPE-2 ANGIOTENSIN II RECEPTOR AND GENE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/148,209A
; FILING DATE: 05-NOV-1993
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I

REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-58491-1/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-148-209A-4

Query Match 100.0%; Score 10; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGKRIQDD 10
DB 8 EDGKRIQDD 17

RESULT 5
US-08-417-122-6
Sequence 6, Application US/08417122
Patent No. 5595882
GENERAL INFORMATION:
APPLICANT: FUJISAWA, Yukio
APPLICANT: KURODA, Shun'ichi
APPLICANT: KONISHI, Hiroaki
TITLE OF INVENTION: ANGIOGENESIS II TYPE-1 RECEPTOR AND ITS
TITLE OF INVENTION: PRODUCTION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEGNER, CANTOR, MUELLER & PLAYER
STREET: 1233 20th Street, N.W., Suite 300
CITY: Washington
STATE: D.C. A.
COUNTRY: U.S.A.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,122
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/041,219
FILING DATE: 31-MAR-1993
APPLICATION NUMBER: JP 085445-1992
FILING DATE: 07-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 101393-1992
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 027835-1993
FILING DATE: 17-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Douglas P.
REGISTRATION NUMBER: 30,300
REFERENCE/DOCKET NUMBER: P-8700-23781
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-0400
TELEFAX: (202) 835-0605
TELEX: 440706
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Placental
US-08-417-122-6

Query Match 100.0%; Score 10; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGKRIQDD 10
DB 8 EDGKRIQDD 17

RESULT 6
US-08-934-222-104
Sequence 104, Application US/08934222
Patent No. 5528896
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interacti
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,222
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-934-222-104

Query Match 70.0%; Score 7; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 IKRIQDD 10
DB 3 IKRIQDD 9

RESULT 7
US-08-933-402-104
; Sequence 104, Application US/08933402
; Patent No. 5948887
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,402
; FILING DATE: 19-SEPT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-933-402-104
Query Match 70.0%; Score 7; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 IKRIODD 10
DB 3 IKRIODD 9
RESULT 8
US-09-207-621-104
; Sequence 104, Application US/09207621
; Patent No. 5952465
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/207,621
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-207-621-104
Query Match 70.0%; Score 7; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 IKRIODD 10
DB 3 IKRIODD 9
RESULT 9
US-08-532-818-104
; Sequence 104, Application US/08532818
; Patent No. 5965698
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interacti
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993

ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-532-818-104

Query Match 70.0%; Score 7; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 IKRIODD 10
DB 3 IKRIODD 9

RESULT 10
US-09-231-797-104
Sequence 104, Application US/09231797
Patent No. 6084066
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
CONSTRAINING GROUPS THAT INCLUDE A PROTEIN-PROTEIN INTERACTION
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,797
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-231-797-104

Query Match 70.0%; Score 7; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 IKRIODD 10
DB 3 IKRIODD 9

DB 3 IKRIODD 9

RESULT 11
US-08-934-224-104
Sequence 104, Application US/08934224
Patent No. 610004
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
CONSTRAINING GROUPS THAT INCLUDE A PROTEIN-PROTEIN INTERACTI
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,224
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-934-224-104

Query Match 70.0%; Score 7; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 IKRIODD 10
DB 3 IKRIODD 9

RESULT 12
US-08-933-843-104
Sequence 104, Application US/08933843
Patent No. 6111069
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
CONSTRAINING GROUPS THAT INCLUDE A PROTEIN-PROTEIN INTERACTI
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner

STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,843
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-933-843-104

Query Match 70.0%; Score 7; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.059; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 IKRIODD 10
DB 3 IKRIODD 9

RESULT 13
US-08-934-223-104
Sequence 104, Application US/08934223
Patent No. 6147189
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,223
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-934-223-104

Query Match 70.0%; Score 7; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.059; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 IKRIODD 10
DB 3 IKRIODD 9

RESULT 14
US-09-413-492-104
Sequence 104, Application US/09413492
Patent No. 6258550
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interacti
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/413,492
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-413-492-104

Query Match 70.0%; Score 7; DB 4; Length 13;
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 Db 3 IKRIODD 9

RESULT 15
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 ; Sequence 10, Application US/09410025
 ; Patent No. 6251623
 ; GENERAL INFORMATION:
 ; APPLICANT: ARAHIRA, MASAO
 ; TITLE OF INVENTION: QUICK ASSAY METHOD FOR THE ACTIVITY OF A PLANT-DERIVED, ASPARAG
 ; FILE REFERENCE: 8361-0008-0
 ; CURRENT APPLICATION NUMBER: US/09/410.025
 ; CURRENT FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: JP10-327536
 ; PRIOR FILING DATE: 1998-11-04
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 10
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 US-09-410-025-10

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 Best Local Similarity 100.0%; Pred. No. 7.4;
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 Db 6 DGIKR 10

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 Job time : 16 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:19:18 ; Search time 10 seconds
(without alignments)
14.419 Million cell updates/sec

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Perfect score: 10
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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	10	100.0	359	10 US-09-867-569-9	Sequence 9, Appl1
2	10	100.0	359	10 US-09-966-871-81	Sequence 81, Appl1
3	10	100.0	359	12 US-10-039-645-81	Sequence 81, Appl1
4	5	50.0	50	10 US-09-764-877-1816	Sequence 116, Ap
5	5	50.0	60	10 US-09-864-761-41362	Sequence 41362, A
6	5	50.0	73	10 US-09-864-761-44645	Sequence 44645, A
7	5	50.0	146	10 US-09-864-761-37689	Sequence 37689, A
8	5	50.0	247	10 US-09-815-242-13461	Sequence 13461, A
9	5	50.0	247	10 US-09-815-242-13622	Sequence 13622, A
10	5	50.0	251	10 US-09-864-761-36797	Sequence 36797, A
11	5	50.0	268	10 US-09-764-853-722	Sequence 722, App
12	5	50.0	296	10 US-09-764-853-480	Sequence 480, App
13	5	50.0	312	10 US-09-925-300-1652	Sequence 1652, Ap
14	5	50.0	318	10 US-09-867-550-1188	Sequence 1188, Ap
15	5	50.0	338	10 US-09-815-242-12043	Sequence 12043, A
16	5	50.0	374	10 US-09-815-242-5579	Sequence 5579, Ap
17	5	50.0	374	10 US-09-815-242-12709	Sequence 12709, A
18	5	50.0	417	9 US-09-879-959-2	Sequence 2, Appl1
19	5	50.0	422	10 US-09-764-864-842	Sequence 842, App

20	5	50.0	422	10 US-09-764-864-1297	Sequence 1297, Ap
21	5	50.0	448	10 US-09-083-002-2	Sequence 2, Appl1
22	5	50.0	448	10 US-09-275-805-2	Sequence 2, Appl1
23	5	50.0	448	10 US-09-836-561-1	Sequence 1, Appl1
24	5	50.0	448	12 US-10-052-586-408	Sequence 408, App
25	5	50.0	457	10 US-09-925-301-1059	Sequence 1059, App
26	5	50.0	579	10 US-09-815-242-11518	Sequence 11518, A
27	5	50.0	632	9 US-09-971-536-42	Sequence 42, Appl1
28	5	50.0	643	10 US-09-815-242-5394	Sequence 5394, Ap
29	5	50.0	657	10 US-09-815-242-12301	Sequence 12301, A
30	5	50.0	710	10 US-09-815-242-10895	Sequence 10895, A
31	5	50.0	773	9 US-09-808-602-60	Sequence 60, Appl1
32	5	50.0	850	9 US-09-808-602-58	Sequence 58, Appl1
33	5	50.0	983	9 US-09-808-602-73	Sequence 73, Appl1
34	4	40.0	17	10 US-09-014-348-4	Sequence 4, Appl1
35	4	40.0	17	10 US-09-782-980-34	Sequence 34, Appl1
36	4	40.0	20	10 US-09-735-705-236	Sequence 236, App
37	4	40.0	20	10 US-09-850-716A-236	Sequence 236, App
38	4	40.0	20	10 US-09-884-441-397	Sequence 397, App
39	4	40.0	20	10 US-09-897-778-236	Sequence 236, App
40	4	40.0	21	10 US-09-735-705-240	Sequence 240, App
41	4	40.0	21	10 US-09-850-716A-240	Sequence 240, App
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43	4	40.0	24	12 US-10-001-879-191	Sequence 191, App
44	4	40.0	30	10 US-09-864-761-48193	Sequence 48193, A
45	4	40.0	32	10 US-09-864-761-46431	Sequence 46431, A

ALIGNMENTS

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RESULT 1
US-09-867-569-9
; Sequence 9, Application US/09867569
; Patent No. US2001003650A1
;
GENERAL INFORMATION:
; APPLICANT: Li et al.
; TITLE OF INVENTION: Csa Receptor
; FILE REFERENCE: PFI30D1C1
; CURRENT APPLICATION NUMBER: US/09/867,569
; CURRENT FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 09/082,529
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: 08/458,970
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/US94/09234
; PRIOR FILING DATE: 1994-08-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 359
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-867-569-9

Query Match          100.0%; Score 10; DB 10; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       8 EDGIRKRIQDD 17

RESULT 2
US-09-966-871-81
; Sequence 81, Application US/09966871
; Patent No. US20020127539A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; TITLE OF INVENTION: Assays for Identifying Receptors Having
; Alterations in Signaling
; FILE REFERENCE: 00398/512002
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; CURRENT APPLICATION NUMBER: US/09/966,871
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,302
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/288,644
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-871-81

Query Match
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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGIRI0DD 10
DB 8 EDGIRI0DD 17

RESULT 3
US-10-039-645-81
; Sequence 81, Application US/10039645
; Patent No. US20020147170A1
; GENERAL INFORMATION:
; APPLICANT: Koplin, Alan S.
; APPLICANT: Belborn, Martin
; TITLE OF INVENTION: Constitutively Active, Hypersensitive,
; FILE REFERENCE: 00398/510002
; CURRENT APPLICATION NUMBER: US/10/039,645
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/243,550
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-645-81

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DB 8 EDGIRI0DD 17

RESULT 4
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; Sequence 1816, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION data removed - refer to PAM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1816
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
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; LOCATION: (4)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (39)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-877-1816

Query Match
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
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; Sequence 41362, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 41362
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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OTHER INFORMATION: MAP TO AL133395.14
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.7
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 6.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.9
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.6
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.8
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6.4
OTHER INFORMATION: SWISSPROT HIT: O31500, EVALU6 6.10e-02
OTHER INFORMATION: EST_HUMAN HIT: D81625.1, EVALU6 2.00e-20
US-09-864-761-41362

Query Match          50.0%; Score 5; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGIK 5
Db 27 EDGIK 31

RESULT 6
US-09-864-761-44645
; Sequence 44645, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
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SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 44645
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC013490.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
; OTHER INFORMATION: EST_HUMAN HIT: H10884.1, EVALU6 9.00e-36
; OTHER INFORMATION: SWISSPROT HIT: P47869, EVALU6 3.00e-39
US-09-864-761-44645

Query Match          50.0%; Score 5; DB 10; Length 73;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 RIQDD 10
Db 62 RIQDD 66

RESULT 7
US-09-864-761-37689
; Sequence 37689, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
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; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 37689
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011422.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN HEEL, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HB1100, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
; OTHER INFORMATION: SWISSPROT HIT: Q16566, EVALUATE 9.00e-58
; OTHER INFORMATION: EST_HUMAN HIT: A1656423.1, EVALUATE 2.00e-56
; US-09-864-761-37689

Query Match          50.0%; Score 5; DB 10; Length 146;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGIR 5
    |||||
Db 95 EDGIR 99

RESULT 8
US-09-815-242-13461
; Sequence 13461, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13461
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
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US-09-815-242-13461
Query Match          50.0%; Score 5; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGIRK 6
    |||||
Db 43 DGIRK 47

RESULT 9
US-09-815-242-13622
; Sequence 13622, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13622
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae

US-09-815-242-13622
Query Match          50.0%; Score 5; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGIRK 6
    |||||
Db 43 DGIRK 47

RESULT 10
US-09-864-761-36797
; Sequence 36797, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aeomica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
```



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; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 36797
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000168.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.84
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.98
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.97
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.96
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 0.75
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.76
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.10e-01
; OTHER INFORMATION: SWISSPROT HIT: P46486, EVALUE 1.10e-01
; OTHER INFORMATION: EST_HUMAN HIT: AW664693.1, EVALUE 2.00e-57
; US-09-864-761-36797
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Query Match          50.0%; Score 5; DB 10; Length 251;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2 DGIKR 6
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Db 19 DGIKR 23
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RESULT 11
; US-09-764-853-722
; Sequence 722, Application US/09764853
; Patent No. US2002090672A1
; GENERAL INFORMATION:
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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 722
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-764-853-722
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Query Match          50.0%; Score 5; DB 10; Length 268;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 EDGIK 5
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Db 43 EDGIK 47
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RESULT 12
; US-09-764-853-480
; Sequence 480, Application US/09764853
; Patent No. US2002090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 480
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (20)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-764-853-480
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Query Match          50.0%; Score 5; DB 10; Length 296;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 EDGIK 5
    |||||
Db 71 EDGIK 75
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RESULT 13
; US-09-925-300-1652
; Sequence 1652, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P1101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
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; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1652
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (289)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1652

Query Match
Best Local Similarity 50.0%; Score 5; DB 10; Length 312;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KRIQD 9
Db 179 KRIQD 183

RESULT 14
US-09-867-550-1188
; Sequence 1188, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehraban, Fuad,
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: NO. US20020082206A1 Polynucleotides from Atherogenic Cells and
; FILE REFERENCE: 21402-013 (Cura-313)
; CURRENT APPLICATION NUMBER: US/09/867,550
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: USSN 60/208,427
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1188
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-867-550-1188

Query Match
Best Local Similarity 50.0%; Score 5; DB 10; Length 318;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 IKRIQ 8
Db 136 IKRIQ 140

RESULT 15
US-09-815-242-12043
; Sequence 12043, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
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; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12043
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-12043

Query Match
Best Local Similarity 50.0%; Score 5; DB 10; Length 338;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KRIQD 9
Db 279 KRIQD 283
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Search completed: November 12, 2002, 16:21:07
Job time : 10 secs

GenCore version 5.1.3
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OW protein - protein search, using sw model

Run on: November 12, 2002, 16:17:58 : Search time 32 seconds
(without alignments)
64.390 Million cell updates/sec

Title: US-09-540-816-1
Perfect score: 10
Sequence: 1 EDGIRIQQDD 10

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp Unclassified:*
- 15: sp_virus:*
- 16: sp_bacterioph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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2	10	100.0	359	4	Q8TBK4	Q8TBK4 homo sapien
3	10	100.0	359	6	Q9GLN9	Q9GLN9 pan troglod
4	10	100.0	359	6	Q9N0U1	Q9N0U1 ovis aries
5	9	90.0	359	11	Q9EP33	Q9EP33 cavia porce
6	6	60.0	62	10	Q9SV77	Q9SV77 arabidopsis
7	6	60.0	126	2	Q51511	Q51511 pseudomonas
8	6	60.0	146	16	Q8REPI	Q8REPI fusobacteri
9	6	60.0	254	17	Q58498	Q58498 methanococ
10	6	60.0	287	16	Q8RA85	Q8RA85 thermoaer
11	6	60.0	348	10	Q41491	Q41491 solanum tub
12	6	60.0	351	16	Q8RI88	Q8RI88 fusobacteri
13	6	60.0	426	16	Q9K8K2	Q9K8K2 bacillus ha
14	6	60.0	442	5	Q9V4A0	Q9V4A0 dirosophila
15	6	60.0	447	16	Q9HUC5	Q9HUC5 pseudomonas
16	6	60.0	472	5	O45259	O45259 caenorhabdi

17	6	60.0	474	2	Q93CD6	Q93CD6 staphylococ
18	6	60.0	477	2	Q8V1X1	Q8V1X1 staphylococ
19	6	60.0	489	16	Q932D7	Q932D7 staphylococ
20	6	60.0	504	10	Q41485	Q41485 solanum tub
21	6	60.0	509	5	Q9VBP6	Q9VBP6 dirosophila
22	6	60.0	509	6	Q9GMC7	Q9GMC7 bison bison
23	6	60.0	656	5	Q9V4E8	Q9V4E8 dirosophila
24	6	60.0	1148	3	Q9P857	Q9P857 phaeosphaer
25	6	60.0	1166	10	Q9ZCE4	Q9ZCE4 arabidopsis
26	6	60.0	1214	12	Q9IN11	Q9IN11 banana virus
27	6	60.0	1219	12	Q9IM03	Q9IM03 banana virus
28	6	60.0	1230	5	Q9NG20	Q9NG20 plasmodium
29	6	60.0	1230	5	Q9XZJ6	Q9XZJ6 plasmodium
30	6	60.0	1680	4	Q9P129	Q9P129 homo sapien
31	5	50.0	21	2	Q9R4V4	Q9R4V4 lactococcus
32	5	50.0	32	16	Q9KPN9	Q9KPN9 vibrio chol
33	5	50.0	61	15	Q89143	Q89143 visna virus
34	5	50.0	62	12	Q8V9Q7	Q8V9Q7 sulfolobus
35	5	50.0	65	2	Q48776	Q48776 listeria mo
36	5	50.0	65	16	Q9RDI7	Q9RDI7 streptomyce
37	5	50.0	73	2	Q8JP52	Q8JP52 helicobacte
38	5	50.0	73	2	Q9JP51	Q9JP51 helicobacte
39	5	50.0	73	2	Q8RS20	Q8RS20 helicobacte
40	5	50.0	73	2	Q8RS18	Q8RS18 helicobacte
41	5	50.0	73	2	Q8RS16	Q8RS16 helicobacte
42	5	50.0	73	2	Q8RS15	Q8RS15 helicobacte
43	5	50.0	73	2	Q8RS10	Q8RS10 helicobacte
44	5	50.0	73	2	Q8RS09	Q8RS09 helicobacte
45	5	50.0	73	2	Q8RS07	Q8RS07 helicobacte

ALIGNMENTS

RESULT 1

Q9QW32 ID Q9QW32 PRELIMINARY: PRT: 343 AA.

AC Q9QW32: MEDLINE=93176370; PubMed=1290618;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Angiotensin receptor AT1.

OS Rattus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10118;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93176370; PubMed=1290618;

RA Murphy T.J., Takeuchi K., Alexander R.W.,

RT "Molecular cloning of AT1 angiotensin receptors."

RL Am. J. Hypertens. 5:236-236(1992).

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

DR HSSP: P34996: 1DDP.

DR InterPro: IPR000276; GPCR_Rhodopsn.

DR Pfam: PF00001; 7tm_1; 1.

DR PRINTS: PR00237; GPCR_RHODOPSN.

DR PROSITE: PS00237; G-PROTEIN_RECPT_F1_1; 1.

DR PROSITE: PS00262; G-PROTEIN_RECPT_F1_2; 1.

KW G-protein coupled receptor; Glycoprotein; Transmembrane.

SQ SEQUENCE 343 AA: 39155 MW: 2CC6A22004CCA93C CRC64;

Query Match 100.0%; Score 10; DB 11; Length 343;

Best Local Similarity 100.0%; Pred. No. 0.0018;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGIRIQQDD 10

DB 6 EDGIRIQQDD 15

RESULT 2

Q8TBK4
ID Q8TBK4 PRELIMINARY; PRT; 359 AA.
AC Q8TBK4;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Angiotensin receptor 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId-9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: BC022447; AAH2447.1; -.
KM Receptor.
SQ SEQUENCE 359 AA; 41087 MW; AF90BE7F21E911BA CRC64;

Query Match 100.0%; Score 10; DB 4; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGIRKIQDD 10
Db 8 EDGIRKIQDD 17

RESULT 3

Q9GLN9
ID Q9GLN9 PRELIMINARY; PRT; 359 AA.
AC Q9GLN9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Angiotensin II type-1 receptor.
GN AGRI.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxId-9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20469400; PubMed=11013071;
RA Dufour C., Casane D., Denton D., Wicks J., Corvol P.,
RA Jeunemaitre X.;
RT "Human-Chimpanzee DNA sequence variation in the four major genes of
RT the renin angiotensin system.";
RL Genomics 69:14-26(2000).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF193445; AAG28410.1; -.
DR HSSP: P34996; 1DDP.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_RECP_FL_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECP_FL_2; 1.
KM G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 359 AA; 41053 MW; 266133A7A3E911A6 CRC64;

Query Match 100.0%; Score 10; DB 6; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGIRKIQDD 10
Db 8 EDGIRKIQDD 17

RESULT 4

Q9N001

ID Q9N001 PRELIMINARY; PRT; 359 AA.
AC Q9N001;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Angiotensin II type 1 receptor.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxId-9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ADRENAL CORTEX;
RA Bird I.M., Milligan D.S.;
RT "Isolation of a Full Length Ovine Angiotensin II Type-1 Receptor (AT1-
RT R) cDNA.";
RL Endocr. Res. 0:0-0(2000).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF254119; AAF6063.1; -.
DR HSSP: P34996; 1DDP.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_RECP_FL_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECP_FL_2; 1.
KM G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 359 AA; 41062 MW; C07010EDB8110EB CRC64;

Query Match 100.0%; Score 10; DB 6; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGIRKIQDD 10
Db 8 EDGIRKIQDD 17

RESULT 5

Q9EPP3
ID Q9EPP3 PRELIMINARY; PRT; 359 AA.
AC Q9EPP3;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Angiotensin II type 1 receptor.
GN AT1.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathii; Cavidae; Cavia.
OX NCBI_TaxId-10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=GALL BLADDER;
RA Busmann A., Noack T., Zucht HD., Forssmann W.G., Meyer M.;
RT "Isolation of Angiotensin I from human hemofiltrate as a potent
RT modulator of KRP channels.";
RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AJ301623; CAC21550.1; -.
DR HSSP: P34996; 1DDP.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_RECP_FL_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECP_FL_2; 1.
KM G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 359 AA; 41045 MW; D00F4C2C472DB5C CRC64;

Query Match 90.0%; Score 9; DB 11; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.023;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGIRKIDD 10
Db 9 DGIRKIDD 17

RESULT 6

O9SJV7 PRELIMINARY; PRT; 62 AA.
AC O9SJV7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Putative ubiquinol-cytochrome C reductase.
GN AT2G01090.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;

RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldylym C.V.,
RA Buell C.R., Ketchum K.A., Lee J.-J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Sherman A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Niernan W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RA "Sequence and analysis of chromosome II of Arabidopsis thaliana.";
RL Nature 402:761-768(1999).
RN [2]

RN SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shin P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full length cDNA of gene F23H14.6/At2g01090 (GI:5598624).";
RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
RN [3]

RN SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Dale J.M., Gibson H.A., Goldsmith A.D., Jiang P.X., Lee J.M.,
RA Quach H.L., Tang C., Toriumi M., Yu G., Bowser L., Carninci P.,
RA Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Kim C., Koeseema E., Lam B., Lin J.,
RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shin P., Southwick A., Tracy S.E.,
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Full length cDNA of gene F23H14.6/At2g01090 (GI:5598624).";
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AC006837; AF18657.1; -;
DR EMBL; AF360220; AA825930.1; -;
DR EMBL; AY040063; AA64121.1; -;
DR InterPro; IPR003422; UCR_hinge.
DR Pfam; PF02320; UCR_hinge.1.
SQ SEQUENCE 62 AA; 7372 MW; 20A8C3AB38EA085 CRC64;

Query Match 60.0%; Score 6; DB 10; Length 62;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 KRIODD 10
Db 33 KRIODD 38

RESULT 7
O51511 PRELIMINARY; PRT; 126 AA.

ID O51511;
AC O51511;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Phac1, phac2 and phad genes (Fragment).
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=PA01;
RA Steinbuichel A.;
RL Submitted (JUN-1992) to the EMBL/Genbank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=PA01;
RX MEDLINE=93011120; PubMed=1396693;
RA Timm A., Steinbuichel A.;
RT "Cloning and molecular analysis of the poly(3-hydroxyalkanoic acid)
RT gene locus of Pseudomonas aeruginosa PA01.";
RL Eur. J. Biochem. 209:15-30(1992).
DR EMBL; X65592; CAA47149.1; -;
DR HSSP; P32168; 1B94.
FT NON_TER
SQ SEQUENCE 126 AA; 14278 MW; 8ADB40A68733FC43 CRC64;

Query Match 60.0%; Score 6; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGIRK 6
Db 49 EDGIRK 54

RESULT 8

ID Q8REP1 PRELIMINARY; PRT; 146 AA.
AC Q8REP1;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Diamine acetyltransferase (EC 2.3.1.57).
GN FNI1057.
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteria; Fusobacterium.
OX NCBI_TaxID=76856;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC 25586;
RX MEDLINE=21886394; PubMed=11889109;
RA Kapralin V., Anderson I., Ivanova N., Reznik G., Los T., Lykilds A.,
RA Bhattacharya A., Bartman A., Gardner W., Grecklin G., Zhu L.,
RA Vasileva O., Chu L., Kogan Y., Chaga O., Goldsman E., Bernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Fontaine M., Kyriades N., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RT nucleatum strain ATCC 25586.";
RL J. Bacteriol. 184:2005-2018(2002).
DR EMBL; AE010612; AAL95253.1; -;
DR Transfaser; Acyltransferase; Complete proteome.
SQ SEQUENCE 146 AA; 17786 MW; BB35B2848DA73C7B CRC64;

Query Match 60.0%; Score 6; DB 16; Length 146;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GIKRIO 8
Db 33 GIKRIO 8

DB 109 GIKRIQ 114

RESULT 9

Q58498 PRELIMINARY; PRT; 254 AA.

AC Q58498; 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)

DE 01-JUN-2002 (TREMBLrel. 21, last annotation update)

GN Hypothetical protein MJ1098.

OS Methanococcus jannaschii.

OC Archaea; Euryarchaeota; Methanococci; Methanococcales;

OC Methanococcaceae; Methanococcus.

OX NCBI_TaxID=2190;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

RM MEDLINE=96337999; PubMed=8688087;

RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,

RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

RA Overbeek R., Kirnness E.F., Weisscock K.G., Merrick J.M., Glodek A.,

RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

RT "Complete genome sequence of the methanogenic archaeon, Methanococcus

RT jannaschii.";

RT J. Jannasch.

CC -1- SIMILARITY: P.CANADENSIS HYPOTHETICAL 28.1 KDA PROTEIN IN URF

CC 3 REGION AND YEAST PROBABLE TRANSPOSASE IN 21S RNA INTRON.

DR EMBL: U67552; AAB99101.1; -.

DR TIGR: MJ1098; -.

DR InterPro: IPR004860; LAGLIDADG_2.

DR Pfam: PF03161; LAGLIDADG_2; 1.

DR Hypothetical protein; Complete proteome.

RM KW

SEQUENCE 254 AA; 30440 MW; E98B050B1340BF34 CRC64;

Query Match

Best Local Similarity 60.0%; Score 6; DB 17; Length 254;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGIKRI 7

DB 139 DGIKRI 144

RESULT 10

Q8RA85 PRELIMINARY; PRT; 287 AA.

AC Q8RA85; 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, last sequence update)

DE 01-JUN-2002 (TREMBLrel. 21, last annotation update)

DE Transcriptional regulator.

GN RPIR3 OR TTE1343.

OS Thermomicrobacter tengcongensis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;

OC Thermomicrobacteriales; Thermomicrobacteriaceae; Thermomicrobacter.

OX NCBI_TaxID=119072;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MBAT / JCM11007;

RM MEDLINE=21992816; PubMed=11997336;

RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,

RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,

RA Tan H., Chen R., Wang J., Yu J., Yang H.;

RT "A complete sequence of T. tengcongensis genome.";

RL Genome Res. 12:689-700(2002).

DR EMBL: AE013094; AAM24565.1; -.

KW Complete proteome.

SEQ SEQUENCE 287 AA; 31991 MW; 0BD628EBA380443E CRC64;

Query Match

Best Local Similarity 60.0%; Score 6; DB 16; Length 287;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KRIQD 9

DB 8 KRIQD 13

RESULT 11

Q41491 PRELIMINARY; PRT; 348 AA.

AC Q41491; 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)

DE 01-JUN-2002 (TREMBLrel. 21, last annotation update)

DE SNF1-related protein kinase (Fragment).

GN PKIN1.

OS Solanum tuberosum (Potato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

OX NCBI_TaxID=4113;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. DESIREE;

RM MEDLINE=97320459; PubMed=9177310;

RA Man A.L., Purcell P.C., Hannappel U., Halford N.G.;

RT "Potato SNF1-related protein kinase: molecular cloning, expression

RT analysis and peptide kinase activity measurements.";

RL Plant Mol. Biol. 34:31-43(1997).

DR EMBL: X95996; CA65243.1; -.

DR InterPro: IPR000719; Euk_pkinase.

DR InterPro: IPR001772; Kinase_Cterm.

DR InterPro: IPR000449; UBA_domain.

DR Pfam: PF02149; KAI; 1.

DR Pfam: PF00069; KAI; 1.

DR Pfam: PF00627; UBA; 1.

DR Pfam: PF000001; Euk_pkinase; 1.

DR SMART: SM00165; UBA; 1.

DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.

DR KW

FT NON_TER

SEQUENCE 348 AA; 39730 MW; CD1C698795D5C0EE CRC64;

Query Match

Best Local Similarity 60.0%; Score 6; DB 10; Length 348;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KRIQD 10

DB 159 KRIQD 164

RESULT 12

Q8RI8 PRELIMINARY; PRT; 351 AA.

AC Q8RI8; 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, last sequence update)

DE 01-JUN-2002 (TREMBLrel. 21, last annotation update)

DE N-acetylneuraminate synthase (EC 4.1.3.19).

GN FN1684.

OS Fusobacterium nucleatum (subsp. nucleatum).

OC Bacteria; Fusobacteria; Fusobacterium.

OX NCBI_TaxID=76856;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 25586;

RM MEDLINE=21886394; PubMed=11889109;

RA Kapatal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,

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RA Bhattacharya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasileva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
RA Lasen N., D'Souza M., Malunas T., Pusch G., Haselkorn R.,
RA Fomstein M., Kyprides N., Overbeek R.,
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RL nucleatum strain ATCC 25586."
DR J. Bacteriol. 184:2005-2018(2002).
KM EMBL: AE010473; AAL93799.1; -.
SO SEQUENCE 351 AA; 39783 MW; 61B52B4CA6103714 CRC64;

Query Match          60.0%; Score 6; DB 16; Length 351;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGIRK 7
DB 274 DGIRK 279

RESULT 13
O9K8K2 PRELIMINARY; PRT; 426 AA.
AC O9K8K2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Sugar transport system (sugar-binding protein).
GN BH1924.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
MEBLIN=C-2051582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kihara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL: AP001513; BAB05643.1; -.
DR InterPro: IPR000567; SBP_bac.1.
DR Pfam: PF01547; SBP_bacterial_1; 1.
KM Complete proteome.
SO SEQUENCE 426 AA; 48207 MW; 8DA0A58385B20D3E CRC64;

Query Match          60.0%; Score 6; DB 16; Length 426;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 IKRIOD 9
DB 416 IKRIOD 421

RESULT 14
O9V4A0 PRELIMINARY; PRT; 442 AA.
AC O9V4A0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CG1155 protein.
GN CG1155.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
MEBLIN=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,
RA Butris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Chertys J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nussken D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtkars R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003846; AAF59382.1; -.
DR HSSP: P19491; IGR2.
DR FLYbase: FBgn003927; CG11155.
DR InterPro: IPR001320; Ion_glu_receptor.
DR InterPro: IPR001622; K_channel_pore.
DR InterPro: IPR001508; NMDA_receptor.
DR InterPro: IPR001311; SBP_glu_receptor.
DR Pfam: PF00060; lig_chan.1.
DR PRINTS: PR00177; NMDARECEPTOR.
DR ProDom: PD000500; Ion_glu_receptor; 1.
DR SMART: SM00079; PBpe.1.
SO SEQUENCE 442 AA; 50244 MW; C7B8E92A833E754D CRC64;

Query Match          60.0%; Score 6; DB 5; Length 442;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGIR 6
DB 272 EDGIR 277

RESULT 15
O9HUC5 PRELIMINARY; PRT; 447 AA.
AC O9HUC5;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Heat shock protein Hs10.
GN Hs10 OR PA5054.
OS Pseudomonas aeruginosa.

```

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
 Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 Brody L.L., Coulter S.N., Folger K.R., Kas A., Lardig K., Lim R.M.,
 Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 DR EMBL; AE004918; AAC08439.1; -.
 DR HSSP; P32168; 1E94.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR003959; AAA_ATPase_cent.
 DR InterPro; IPR004491; Hsp_HslV.
 DR Pfam; PF00004; AAA; 1.
 DR SMART; SM00382; AAA; 1.
 DR TIGRFAWS; TIGR00390; hslV; 1.
 KW Complete proteome.
 SQ SEQUENCE 447 AA; 50082 MM; BEF52E52A4363043 CRC64;

Query March 60.0%; Score 6; DB 16; Length 447;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EDGIRK 6
 |||||
 Db 370 EDGIRK 375

Search completed: November 12, 2002, 16:20:09
 Job time : 34 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:17:38 ; Search time 11 Seconds
(without alignments)
37.706 Million cell updates/sec

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Title: US-09-540-816-1
Perfect score: 10
Sequence: 1 EDGKRQDD 10
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

word size : 0

Total number of hits satisfying chosen parameters: 112892

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Maximum DB seq length: 20000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	100.0	359	1 AG2R_BOVIN	P25104 bos taurus
2	10	100.0	359	1 AG2R_CANEA	P43324 canis famillia
3	10	100.0	359	1 AG2R_CAVPO	O9wv26 cavia porcea
4	10	100.0	359	1 AG2R_HUMAN	P30536 homo sapien
5	10	100.0	359	1 AG2R_MOUSE	P29754 mus musculu
6	10	100.0	359	1 AG2R_RABIT	P34969 oryctolagus
7	10	100.0	359	1 AG2R_RAT	P25095 rattus norv
8	10	100.0	359	1 AG2S_SHEEP	O77590 ovis aries
9	10	100.0	359	1 AG2S_HUMAN	O13725 homo sapien
10	10	100.0	359	1 AG2S_MOUSE	P29755 mus musculu
11	10	100.0	359	1 AG2S_RAT	P29089 rattus norv
12	9	90.0	359	1 AG2R_MEMUN	O35210 meriones un
13	7	70.0	359	1 AG2R_PIG	P30555 sus scrofa
14	6	60.0	228	1 FLPA_MERVO	P35553 methanococc
15	6	60.0	447	1 HSLU_PSEAE	O9uhcs pseudonasa
16	6	60.0	509	1 CP17_BOVIN	P05185 bov taurus
17	6	60.0	586	1 VGLN_BEVY	P23566 bovine ephne
18	6	60.0	611	1 YCR3_YEAST	P25351 saccharomyc
19	6	60.0	785	1 YHY2_YEAST	P38870 saccharomyc
20	5	50.0	79	1 PSPB_PIG	P15782 sus scrofa
21	5	50.0	91	1 TIM2_HORSE	O77171 equus cabala
22	5	50.0	110	1 KDGF_ERICH	O9u557 eulimnia chr
23	5	50.0	119	1 RL24_SUISO	O9ux95 sulfolobus
24	5	50.0	129	1 YE7B_MERIA	P81227 methanococc
25	5	50.0	132	1 RS8_STROK	P49389 streptomycce
26	5	50.0	140	1 SEDL_HUMAN	O14582 homo sapien
27	5	50.0	140	1 SEDL_MOUSE	O9cqp2 mus musculu
28	5	50.0	145	1 GLB2_LUTTE	P02218 lumbricus t
29	5	50.0	151	1 HSPR_STRCO	P40183 streptomyces
30	5	50.0	174	1 NADM_ARCFU	O27969 archaeoglob
31	5	50.0	185	1 LYG_CYGAT	P00717 cygnus atrat
32	5	50.0	191	1 THGD_BACSU	P32398 bacillus
33	5	50.0	194	1 TIM2_RABIT	O9tltz7 oryctolagus

34	5	50.0	194	1	V615_PTYAB	G9V074 pyrooccus
35	5	50.0	196	1	TIM2_CRIO	O60453 cricetus
36	5	50.0	220	1	TIM2_BOVIN	P16368 bos taurus
37	5	50.0	220	1	TIM2_CANFA	Q9LY1 canis faml
38	5	50.0	220	1	TIM2_CAVPO	Q9WU6 cavia porce
39	5	50.0	220	1	TIM2_CHICK	O42146 gallus gail
40	5	50.0	220	1	TIM2_HUMAN	P16035 homo saplen
41	5	50.0	220	1	TIM2_MOUSE	P25755 mus musculu
42	5	50.0	220	1	TIM2_RAT	P10121 rattus norv
43	5	50.0	221	1	AG14_ARATH	Q38838 arabidopsis
44	5	50.0	225	1	ISPD_CLOPE	O6Xh3 clostridium
45	5	50.0	231	1	MSBB_SHIFL	O06659 shigella fl

ALIGNMENTS

RESULT 1

AG2R_BOVIN

ID	AG2R_BOVIN	STANDARD:	PRT:	359 AA.
AC	P25104;			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-MAY-1992 (Rel. 22, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	Type-1 angiotensin II receptor (ATI).			
GN	AGTRL.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
CC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91251900; PubMed=2041569;			
RA	Sasaki K., Yamano Y., Barchan S., Iwai N., Murray J.J., Hasegawa M.,			
RA	Matsuda Y., Inagami T.,			
RT	"Cloning and expression of a complementary DNA encoding a bovine			
RT	adrenal angiotensin II type-1 receptor.";			
RL	Nature 351:230-233(1991).			
CC	- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY			
CC	ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-			
CC	CALCIUM SECOND MESSENGER SYSTEM.			
CC	- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	- TISSUE SPECIFICITY: ADRENAL MEDULLA, CORTEX, AND KIDNEY.			
CC	- PFM: CARBOXY-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.			
CC	- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	-----			
DR	EMBL; X62294; CAA44182.1; -.			
DR	PIR; S15403; S15403.			
DR	HSSP; P34996; 1DDP.			
DR	InterPro; IPR000276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; 7tm_1.1.			
DR	PRINTS; PR00237; GPCRHHODPSN.			
DR	PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.			
DR	PROSITE; PS02623; G-PROTEIN_RECEP_FL_2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;			
KW	Palmitate; phosphorylation.			
FT	DOMAIN	1	27	EXTRACELLULAR (POTENTIAL).
FT	TRANSMM	28	32	1 (POTENTIAL).
FT	DOMAIN	53	64	CYTOPLASMIC (POTENTIAL).
FT	TRANSMM	65	87	2 (POTENTIAL).
FT	DOMAIN	88	102	EXTRACELLULAR (POTENTIAL).
FT	TRANSMM	103	124	3 (POTENTIAL).
FT	DOMAIN	125	142	CYTOPLASMIC (POTENTIAL).
FT	TRANSMM	143	162	4 (POTENTIAL).

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FT DOMAIN 163 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 214 5 (POTENTIAL).
FT DOMAIN 215 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 241 262 6 (POTENTIAL).
FT DOMAIN 263 275 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 296 7 (POTENTIAL).
FT DOMAIN 297 359 359 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 101 180 BY SIMILARITY.
FT LIPID 355 355 PALMITATE (POTENTIAL).
SQ SEQUENCE 359 AA; 41088 MW; B426BFF6B61DFA CRC64;

Query Match
Best Local Similarity 100.0%; Score 10; DB 1; Length 359;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGIRRIODD 10
DB 8 EDGIRRIODD 17

RESULT 2
AG2R_CANFA STANDARD: PRT: 359 AA.
ID AG2R_CANFA
AC P43240;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Type-1 angiotensin II receptor (AT1).
GN AGTRL.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN NCBI_TaxID=9615;
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94222188; PubMed=8168620;
RA Burns L., Clark K.L., Bradley J., Robertson M.J., Clark A.J.;
RT "Molecular cloning of the canine angiotensin II receptor. An AT1-like
RL receptor with reduced affinity for Dnp753."
CC -1- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: ADRENAL, LIVER, AORTA, KIDNEY, LUNG, TESTIS
CC AND HEART.
CC -1- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR HSSP: P34996: 1DD.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_REC_P1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_REC_P1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
KW Palmitate; Phosphorylation.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 52 1 (POTENTIAL).
FT DOMAIN 53 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 87 2 (POTENTIAL).
FT DOMAIN 88 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 142 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 143 162 4 (POTENTIAL).
FT DOMAIN 163 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 214 5 (POTENTIAL).
FT DOMAIN 215 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 241 262 6 (POTENTIAL).
FT DOMAIN 263 275 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 276 296 7 (POTENTIAL).
FT DOMAIN 297 359 359 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 101 180 BY SIMILARITY.
FT LIPID 355 355 PALMITATE (POTENTIAL).
SQ SEQUENCE 359 AA; 40901 MW; 22A1BADFABDAD50E CRC64;

Query Match
Best Local Similarity 100.0%; Score 10; DB 1; Length 359;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGIRRIODD 10
DB 8 EDGIRRIODD 17

RESULT 3
AG2R_CAVPO STANDARD: PRT: 359 AA.
ID AG2R_CAVPO
AC O9WY26;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Type-1 angiotensin II receptor (AT1).
GN AGTRL.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN NCBI_TaxID=10141;
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley; TISSUE=Liver;
RX MEDLINE=20423173; PubMed=10965057;
RA Hosoda Y., Fujino I., Akagawa K., Kuwahara A.;
RT "Molecular cloning of guinea pig angiotensin type 1 receptor."
RL Biol. Signals Recept. 9:231-239(2000).
CC -1- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL: AF165888; AAD45383.1; -.
DR HSSP: P34996: 1DD.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_REC_P1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_REC_P1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
KW Palmitate; Phosphorylation.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 52 1 (POTENTIAL).
FT DOMAIN 53 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 87 2 (POTENTIAL).
FT DOMAIN 88 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 142 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 143 162 4 (POTENTIAL).
FT DOMAIN 163 192 5 (POTENTIAL).
FT TRANSMEM 193 214 5 (POTENTIAL).
FT DOMAIN 215 240 CYTOPLASMIC (POTENTIAL).

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FT TRANSMEM 241 262 6 (POTENTIAL).
FT DOMAIN 263 275 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 296 7 (POTENTIAL).
FT DOMAIN 297 359 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 101 180 BY SIMILARITY.
FT LIPID 355 355 PALMITATE (POTENTIAL).
SQ SEQUENCE 359 AA; 40985 MW; 11991138FP81C19 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGKRRDOD 10
   |||||
Db 8 EDGKRRDOD 17

RESULT 4
AG2R HUMAN STANDARD; PRT; 359 AA.
AC P30556;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Type-1 angiotensin II receptor (AT1) (A1IAR).
GN AGT1R OR AGT1RA OR AT2R1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=92337608; PubMed=1378723;
RA Maury C.A., Hwang O., Eglolf A.M., Wu L.H., Chung F.-Z.;
RT "Cloning, expression, and characterization of a gene encoding the
RL human angiotensin II type 1A receptor.";
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes; PubMed=1543512;
RA Furtta H., Guo D.F., Inagami T.;
RT "Molecular cloning and sequencing of the gene encoding human
RL angiotensin II type 1 receptor.";
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver; PubMed=1567413;
RA Bergsma D.J., Ellis C., Kumar C., Nuthalaganti P., Kersten H.,
RT Elshoutbagy N.A., Griffin E., Stadel J.M., Aiyar N.;
RT "Cloning and characterization of a human angiotensin II type 1
RL receptor.";
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver; PubMed=1550596;
RA Inagami T., Furtta H., Gou D.F., Nakanata M., Nawata H.;
RT "Molecular cloning, sequence analysis and expression of a cDNA
RL encoding human type-1 angiotensin II receptor.";
RN [5]
RP SEQUENCE FROM N.A.
RC MEDLINE=92375105; PubMed=1508224;
RA Curnow K.M., Pascoe L., White P.C.;
RT "Genetic analysis of the human type-1 angiotensin II receptor.";
RN [6]

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RP SEQUENCE FROM N.A.
RC TISSUE=Liver; PubMed=7792812;
RA MEDLINE=95313084; PubMed=7792812;
RA Nawata H., Takayanagi R., Ohnaka K., Sakai Y., Imasaki K., Yanase T.,
RA Ikuyama S., Tanaka S., Ohe K.;
RT "Type 1 angiotensin II receptors of adrenal tumors.";
RN [7]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Ostermann E., Castanon M.J.;
RN Submitted (XX-1995) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RA Antocellis A., Rogus J.J., Pezolesi M.G., Makita Y., Nam M.,
RA Doria A., Warram J.H., Krolewski A.S.;
RT "Rapid identification of polymorphisms in genomic DNA: a high density
RT SNP map of the type 1 angiotensin II receptor gene locus on chromosome
RT 3q.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC -! SUBCELLULAR LOCATION: Integral membrane protein.
CC -! TISSUE SPECIFICITY: LIVER, LUNG, ADRENAL, AND ADRENOCORTICAL
CC ADENOMAS.
CC -! PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
CC -! SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M91464; AAA35569.1; -
DR EMBL; Z1162; CAA77513.1; -
DR EMBL; M87290; AAA35535.1; -
DR EMBL; M83394; AAB58370.1; -
DR EMBL; S77410; AAB34644.1; -
DR EMBL; X65699; CAA46621.1; -
DR EMBL; AF245699; AAF70464.1; -
DR PIR; A44014; A44014.
DR PIR; JC1104; JC1104.
DR HSSP; P34996; 1DDP.
DR Genew; HGNC:336; AGT1R.
DR MIM; 106165; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECPT_FL_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
KW Palmitate; Phosphorylation; Polymorphism.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 52 1 (POTENTIAL).
FT DOMAIN 53 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 87 2 (POTENTIAL).
FT DOMAIN 88 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 142 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 143 162 4 (POTENTIAL).
FT DOMAIN 163 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 214 5 (POTENTIAL).
FT DOMAIN 215 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 241 262 6 (POTENTIAL).
FT DOMAIN 263 275 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 296 7 (POTENTIAL).
FT DOMAIN 297 359 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 101 180 BY SIMILARITY.
FT LIPID 355 355 PALMITATE (POTENTIAL).
FT VARIANT 48 48 L -> V (IN DBSNP:2011425).
FT VARIANT 289 289 /FTID=VAR_011846.
FT VARIANT 289 289 C -> W (IN DBSNP:1064533).
FT VARIANT 336 336 /FTID=VAR_011847.
FT VARIANT 336 336 T -> P (IN DBSNP:1801021).
FT SEQUENCE 359 AA; 41061 MW; 35FC856F53E911A6 CRC64;
SO

Query Match 100.0%; Score 10; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGIKRIODD 10
Db 8 EDGIKRIODD 17

RESULT 5
AG2R_MOUSE
ID AG2R_MOUSE STANDARD: PRT; 359 AA.
IC P29754;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Type-1A angiotensin II receptor (AT1A).
GN ACT1A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=92287102; PubMed=159461;
RA Sasamura H., Hein L., Krieger J.E., Pratt R.E., Koblika B.K.,
RA Dzeu V.J.;
RT "Cloning, characterization, and expression of two angiotensin
RT receptor (AT-1) isoforms from the mouse genome."
RL Biochem. Biophys. Res. Commun. 185:253-259(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92359981; PubMed=1497638;
RA Yoshida H., Kakuchi J., Guo D.F., Furuta H., Iwai N.,
RA van der Meer-De Jong R., Inagami T., Ichikawa I.;
RT "Analysis of the evolution of angiotensin II type 1 receptor gene in
RT mammals (mouse, rat, bovine and human).";
RL Biochem. Biophys. Res. Commun. 186:1042-1049(1992).
CC -1- FUNCTION: RECEPTOR FOR ANGIOGENSIN II. MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIN SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL, S37484; AB022269.1; -
DR PIR, JH0621; JH0621.
DR PIR, JC1193; JC1193.
DR HSSP; P34996; 1DDO.
DR MGD; MGI:87964; Act1a
DR InterPro, IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.

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DR	PROSITE; PS00237; G-PROTEIN_RECCEP_FL_1; 1.
DR	PROSITE; PSS0262; G-PROTEIN_RECCEP_FL_2; 1.
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
RK	Palmitate; Phosphorylation.
FT	DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT	TRANSMM 28 52 1 (POTENTIAL).
FT	DOMAIN 53 64 CYTOPLASMIC (POTENTIAL).
FT	TRANSMM 65 87 2 (POTENTIAL).
FT	DOMAIN 88 102 EXTRACELLULAR (POTENTIAL).
FT	TRANSMM 103 124 3 (POTENTIAL).
FT	DOMAIN 125 142 CYTOPLASMIC (POTENTIAL).
FT	TRANSMM 143 162 4 (POTENTIAL).
FT	DOMAIN 163 192 EXTRACELLULAR (POTENTIAL).
FT	TRANSMM 193 214 5 (POTENTIAL).
FT	DOMAIN 215 240 CYTOPLASMIC (POTENTIAL).
FT	TRANSMM 241 262 6 (POTENTIAL).
FT	DOMAIN 263 275 EXTRACELLULAR (POTENTIAL).
FT	TRANSMM 276 296 7 (POTENTIAL).
FT	DOMAIN 297 359 CYTOPLASMIC (POTENTIAL).
FT	CARBOHD 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFD 101 180 BY SIMILARITY.
FT	LIPID 355 355 PALMITATE (POTENTIAL).
FT	CONFLICT 7 T -> I (IN REF. 2).
FT	CONFLICT 20 RA -> IS (IN REF. 2).
FT	CONFLICT 38 I -> M (IN REF. 2).
FT	CONFLICT 134 M -> K (IN REF. 2).
FT	CONFLICT 134
SQ	SEQUENCE 359 AA; 40855 MW; 966958A78DBF53E CnC64;
<hr/>	
Query Match Best Local Similarity 100.0%; Score 10; DB 1; Length 359;	
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0.	
OY	1 EDGIRIODD 10
Dd	8 EDGIRIODD 17
<hr/>	
RESULT 6 AGZR_RABIT	
ID	AGZR_RABIT STANDARD; PRT; 359 AA.
AC	P34976;
DT	01-FEB-1994 (Rel. 28, Created)
DT	01-FEB-1994 (Rel. 28, Last sequence update)
DT	01-NOV-1997 (Rel. 35, Last annotation update)
DE	Type-1 angiotensin II receptor (AT1).
GN	AGTRL.
OS	Oryctolagus cuniculus (Rabbit).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX	NCBI_Taxid=9986;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Kidney;
RC	MEDLINE=93236091; PubMed=7916579;
RX	Burns K.D., Inagami T., Harris R.C.;
RA	"Cloning of a rabbit kidney cortex AT1 angiotensin II receptor that
RT	is present in proximal tubule epithelium.";
RL	Am. J. Physiol. 264:F645-F654(1993).
CC	-1- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.
CC	-1- PM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
CC	-1- SIMILARITY: BELONGS TO FAMILY I OF G-PROTEIN COUPLED RECEPTORS.
CC	-----
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CC EMBL; S59041; AAB26239.1; -.
DR PIR; A48857; A48857.
DR HSSP; P34996; 1DDP.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN_RECP_FL_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
KW Palmitate; Phosphorylation.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 52 1 (POTENTIAL).
FT TRANSMEM 53 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 87 2 (POTENTIAL).
FT TRANSMEM 88 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT TRANSMEM 125 142 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 143 162 4 (POTENTIAL).
FT TRANSMEM 163 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 214 5 (POTENTIAL).
FT TRANSMEM 215 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 241 262 6 (POTENTIAL).
FT TRANSMEM 263 275 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 296 7 (POTENTIAL).
FT TRANSMEM 297 359 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 101 180 BY SIMILARITY.
FT LIPID 355 PALMITATE (POTENTIAL).
SQ SEQUENCE 359 AA; 40989 MW; C27AC1A2BB6AD576 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGKRIQDD 10
Db 8 EDGKRIQDD 17

RESULT 7
AC2R_RAT STANDARD; PRT; 359 AA.
AC P25095; Q9QV55;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Type-1A angiotensin II receptor (AT1A).
GN AGT1RA OR AT1A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Vascular smooth muscle;
RX MEDLINE-91251901; PubMed=2041570;
RA Murphy T.J., Alexander R.W., Griendling K.K., Runge M.S.,
RA Bernstein K.E.;
RT "Isolation of a cDNA encoding the vascular type-1 angiotensin II
RT receptor.";
RL Nature 351:233-236(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Kidney;
RX MEDLINE-91254291; PubMed=2043116;
RA Iwai N., Yamano Y., Chaki S., Konishi F., Bardhan S., Tibbetts C.,
RA Sasaki K., Hasegawa M., Matsuda Y., Inagami T.;
RT "Rat angiotensin II receptor: cDNA sequence and regulation of the
RT gene expression.";

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RL Biochem. Biophys. Res. Commun. 177:299-304(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-92231859; PubMed=1533121;
RA Langford K.G., Frenzel K., Martin B.M., Bernstein K.E.;
RT "The genomic organization of the rat AT1 angiotensin receptor.";
RL Biochem. Biophys. Res. Commun. 183:1025-1032(1992).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE-95228708; PubMed=7713098;
RA Inagami T., Iwai N., Sasaki K., Yamano Y., Bardhan S., Chaki S.,
RA Guo D.F., Furuta H., Ohyama K., Kamabayashi Y.;
RT "Cloning, expression and regulation of angiotensin II receptors.";
RL Eur. Heart J. 15:104-107(1994).
CC -1- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC LUNG, UTERUS, OVARY, SPLEEN, HEART, ADRENAL GLAND, AND VASCULAR
CC SMOOTH MUSCLE CELL.
CC -1- PTM: CARBOXY-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; X62295; CAA44183.1; -.
DR EMBL; M74054; AAA40738.1; -.
DR EMBL; M86912; -. NOT_ANNOTATED_CDS.
DR PIR; JQ1055; JQ1055.
DR PIR; S15404; S15404.
DR PIR; S20424; S20424.
DR PIR; JC2134; JC2134.
DR HSSP; P34996; 1DDP.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN_RECP_FL_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
KW Palmitate; Phosphorylation.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 52 1 (POTENTIAL).
FT TRANSMEM 53 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 87 2 (POTENTIAL).
FT TRANSMEM 88 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT TRANSMEM 125 142 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 143 162 4 (POTENTIAL).
FT TRANSMEM 163 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 214 5 (POTENTIAL).
FT TRANSMEM 215 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 241 262 6 (POTENTIAL).
FT TRANSMEM 263 275 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 296 7 (POTENTIAL).
FT TRANSMEM 297 359 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 101 180 BY SIMILARITY.
FT LIPID 355 PALMITATE (POTENTIAL).
FT CONFLICT 81 L -> C (IN REF. 2).
FT CONFLICT 109 S -> T (IN REF. 2 AND 4).
SQ SEQUENCE 359 AA; 40989 MW; 200EAB56BD4D678 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.00018;

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	Matches	10;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	EDGIRKIODD	10							
Db	8	EDGIKRIODD	17							
	RESULT 8									
ID	AG2R_SHEEP	STANDARD;	PRT;	359 AA.						
AC	077590;									
DT	16-OCT-2001 (Rel. 40, Created)									
DF	16-OCT-2001 (Rel. 40, Last sequence update)									
DT	16-OCT-2001 (Rel. 40, Last annotation update)									
DE	Type-1 angiotensin II receptor (AT1).									
GN	AGTRL.									
OS	Ovis aries (Sheep).									
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
CC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;									
CC	Bovidae; Caprinae; Ovis.									
OX	NCB1_TaxID=9940;									
RN	(1)									
RP	SEQUENCE FROM N.A.									
RX	MEDLINE=99103586; PubMed=9888511;									
RA	Millikan D.S.; Bird I.M.;									
RT	"Isolation of an ovine genomic sequence containing the full-length									
RL	angiotensin II type-1 receptor.";									
RN	Endocr. Res. 24:387-390(1998).									
RP	[2]									
RC	SEQUENCE OF 1-132 FROM N.A.									
RX	TISSUE=Adrenal cortex;									
RA	MEDLINE=98351904; PubMed=9687288;									
RT	Bird I.M., Millikan D.S., Magness R.R.;									
RL	"Specific pregnancy-induced angiotensin II type-1 receptor expression									
RT	in ovine uterine artery does not involve formation of alternate splice									
RL	variants or alternate promoter usage."									
CC	Biol. Reprod. 59:219-224(1998).									
CC	- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY									
CC	ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-									
CC	CALCIUM SECOND MESSENGER SYSTEM.									
CC	- SUBCELLULAR LOCATION: Integral membrane protein.									
CC	- PFM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.									
CC	- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.									
CC	-----									
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CC	or send an email to license@sdb.ch).									
CC	-----									
DR	EMBL: AF069750; AAC9344.1; -									
DR	EMBL: AF056308; AAC32613.1; -									
DR	HSSP: P34396; 1DDP									
DR	InterPro; IPR000276; GPCR_Rhodpsn.									
DR	Pfam; PF00001; 7tm_1; 1.									
DR	PRINTS; PR00237; GPCRHHODPSN.									
DR	PROSITE; PS00237; G_PROTEIN_REC_P1_1; 1.									
DR	PROSITE; PS00262; G_PROTEIN_REC_P1_2; 1.									
KM	G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;									
KW	Dominate; Phosphorylation.									
FT	DOMAIN	1	27							
FT	TRANSMEM	28	52							
FT	DOMAIN	53	64							
FT	TRANSMEM	65	87							
FT	DOMAIN	88	102							
FT	TRANSMEM	103	124							
FT	DOMAIN	125	142							

FT	TRANSMEM	241	262		6 (POTENTIAL).
FT	DOMAIN	263	275		EXTRACELLULAR (POTENTIAL).
FT	TRANSEM	276	296		7 (POTENTIAL).
FT	DOMAIN	297	359		CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	4	4		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	176	176		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	188	188		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	101	180		BY SIMILARITY.
FT	LIPID	355	355		PALMITATE (POTENTIAL).
SO	SEQUENCE	359 AA;	41046 MW;	c07010f1a4110c67 cnc64;	
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Query Match		100.0%;	Score 10;	DB 1;	Length 359;
Best Local Similarity		100.0%;	Pred. No. 0.00018;		
Matches	10; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;
OY	1 EDGIKRIODD 10				
Db	8 EDGIKRIODD 17				
<hr/>					
RESULT 9					
AG2S_HUMAN	STANDARD:	PRT;	359 AA.		
ID AG2S_HUMAN	Q13725;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Type-1B angiotensin II receptor (AT1B) (A11BR).				
GN	ACTR1B OR AT2R1B.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Placenta;				
RX	MEDLINE=94183213; PubMed=8135787;				
RA	Konishi H., Kuroda S., Inada Y., Fujisawa Y.;				
RT	"Novel subtype of human angiotensin II type I receptor: CDNA cloning and expression.";				
RL	Biochem. Biophys. Res. Commun. 199;467-474(1994).				
CC	- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.				
CC	- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	- TISSUE SPECIFICITY: EXPRESSED IN THE LUNG, PLACENTA AND LIVER.				
CC	- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.				
CC	- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
CC	-----				
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CC	-----				
DR	EMBL; D13814; BAA02968.1; -.				
DR	HSSP; P34996; 1DD.				
DR	InterPro; IPR000276; GPCR_rhodpsn.				
DR	pfam; PF00001; 7tm1.1; 1.				
DR	PRINTS; PR00237; GPCRRHODPSN.				
DR	PROSITE; PS00237; G_PROTEIN_REC_F1_1; 1.				
DR	PROSITE; PS50562; G_PROTEIN_REC_F1_2; 1.				
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein; Palmitate; Phosphorylation.				
FT	DOMAIN	1	27		EXTRACELLULAR (POTENTIAL).
FT	TRANSEM	28	52		1 (POTENTIAL).
FT	DOMAIN	53	64		CYTOPLASMIC (POTENTIAL).
FT	TRANSEM	65	87		2 (POTENTIAL).
FT	DOMAIN	88	102		EXTRACELLULAR (POTENTIAL).
FT	TRANSEM	103	124		3 (POTENTIAL).
FT	DOMAIN	125	142		CYTOPLASMIC (POTENTIAL).

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FT TRANSMEM 143 162 4 (POTENTIAL).
FT DOMAIN 163 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 214 5 (POTENTIAL).
FT TRANSMEM 215 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 241 262 6 (POTENTIAL).
FT TRANSMEM 263 275 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 296 7 (POTENTIAL).
FT TRANSMEM 297 359 7 (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT DISULFID 101 180 BY SIMILARITY.
FT LIPID 355 355 PALMITATE (POTENTIAL).
SQ SEQUENCE 359 AA; 41020 MW; 2989FD3FE50D4EA4 CRC64;

Query Match
Best Local Similarity 100.0%; Score 10; DB 1; Length 359;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGIRKIQDD 10
DB 8 EDGIRKIQDD 17

RESULT 10
AG2S_MOUSE STANDARD; PRT; 359 AA.
ID AG2S_MOUSE STANDARD; PRT; 359 AA.
AC P29755;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Type-1b angiotensin II receptor (AT1b) (AT3).
GN AGTR1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/c; TISSUE-Liver;
RX MEDLINE=92287102; PubMed=1599461;
RA Sasamura H., Hein L., Krieger J.E., Pratt R.E., Koblika B.K.,
RA Dzaou V.J.;
RT "Cloning, characterization, and expression of two angiotensin
RT receptor (AT-1) isoforms from the mouse genome.";
RL Biochem. Biophys. Res. Commun. 185:253-259(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9235981; PubMed=1497638;
RA Yoshida H., Kakuchi J., Guo D.F., Furuta H., Iwai N.,
RA van der Meer-De Jong R., Inagami T., Ichikawa I.;
RT "Analysis of the evolution of angiotensin II type 1 receptor gene in
RT mammals (mouse, rat, bovine and human).";
RL Biochem. Biophys. Res. Commun. 186:1042-1049(1992).
CC -I- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC -----
CC EMBL: S37491; AAB22270.1; -
CC PIR: JH0622; JH0622.
CC PIR: JC1194; JC1194.
CC HSP: P34996; 1DD0.

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DR MGD; MGI:87965; Agtr1b.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_Rhodpsn.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
KW Palmitate; Phosphorylation.
FT TRANSMEM 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 52 1 (POTENTIAL).
FT TRANSMEM 53 64 1 (POTENTIAL).
FT TRANSMEM 65 87 2 (POTENTIAL).
FT TRANSMEM 88 102 2 (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT TRANSMEM 125 142 3 (POTENTIAL).
FT TRANSMEM 143 162 4 (POTENTIAL).
FT TRANSMEM 163 192 4 (POTENTIAL).
FT TRANSMEM 193 214 5 (POTENTIAL).
FT TRANSMEM 215 240 6 (POTENTIAL).
FT TRANSMEM 241 262 6 (POTENTIAL).
FT TRANSMEM 263 275 7 (POTENTIAL).
FT TRANSMEM 276 296 7 (POTENTIAL).
FT TRANSMEM 297 359 7 (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT DISULFID 101 180 BY SIMILARITY.
FT LIPID 355 355 PALMITATE (POTENTIAL).
FT CONFLICT 7 7 I -> T (IN REF. 2).
FT CONFLICT 166 166 H -> Y (IN REF. 2).
FT CONFLICT 173 173 E -> A (IN REF. 2).
FT CONFLICT 205 205 V -> E (IN REF. 2).
FT CONFLICT 232 232 T -> I (IN REF. 2).
FT CONFLICT 239 239 F -> G (IN REF. 2).
SQ SEQUENCE 359 AA; 40949 MW; 95730F97058EAA4B CRC64;

Query Match
Best Local Similarity 100.0%; Score 10; DB 1; Length 359;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGIRKIQDD 10
DB 8 EDGIRKIQDD 17

RESULT 11
AG2S_RAT STANDARD; PRT; 359 AA.
ID AG2S_RAT STANDARD; PRT; 359 AA.
AC P29089;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Type-1b angiotensin II receptor (AT1b) (AT3).
GN AGTR1B OR AT1B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley;
RX MEDLINE=92183879; PubMed=1544458;
RA Iwai N., Inagami T.;
RT "Identification of two subtypes in the rat type I angiotensin II
RT receptor.";
RL FEBS Lett. 298:257-260(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Adrenal cortex;
RX MEDLINE=92250585; PubMed=1374402;
RA Sandberg K., Ji H., Clark A.J., Shapira H., Catt K.J.;
RT "Cloning and expression of a novel angiotensin II receptor subtype.";
RL J. Biol. Chem. 267:9455-9458(1992).

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RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Anterior pituitary;
RX MEDLINE=92231868; PubMed=1567388;
RA Kakar S.S., Sellers J.C., Devor D.C., Musgrove L.C., Neill J.D.;
RT "Angiotensin II type-1 receptor subtype cDNAs: differential tissue
RL Biochem. Biophys. Res. Commun. 183:1090-1096(1992).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=92246922; PubMed=1575725;
RA Elton T.S., Stephan C.C., Taylor G.R., Kimball M.G., Martin M.M.,
RA Durand J.N., Oparil S.;
RT "Isolation of two distinct type I angiotensin II receptor genes.";
RL Biochem. Biophys. Res. Commun. 184:1067-1073(1992).
CC -1- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: IS EXPRESSED IN THE LIVER, KIDNEY, AORTA,
CC LUNG, UTERUS, OVARY, SPLEEN, HEART, ADRENAL GLAND, AND VASCULAR
CC SMOOTH MUSCLE CELL.
CC -1- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL: X64052; CAA45410.1; -
DR EMBL: M90065; AAA40704.1; -
DR EMBL: M87003; AAA40739.1; -
DR PIR: A42656; A42656.
DR PIR: S20423; S20423.
DR PIR: JH0578; JH0578.
DR PIR: JQ1516; JQ1516.
DR HSSP: P34996; 1DDP.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOODPSN.
DR PROSITE: PS00237; G_PROTEIN_REC_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_REC_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 52 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 53 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 87 2 (POTENTIAL).
FT DOMAIN 88 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 142 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 143 162 4 (POTENTIAL).
FT DOMAIN 163 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 214 5 (POTENTIAL).
FT DOMAIN 215 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 241 262 6 (POTENTIAL).
FT DOMAIN 263 275 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 296 7 (POTENTIAL).
FT DOMAIN 297 359 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 101 180 BY SIMILARITY.
FT CONFLICT 2 40 T -> I (IN REF. 3 AND 4).
FT CONFLICT 40 40 V -> M (IN REF. 3 AND 4).
FT CONFLICT 75 75 L -> Y (IN REF. 4).
SQ SEQUENCE 359 AA; 40911 MW; A2CC21E0B365C5B CRC64;
Query Match 100.0%; Score 10; DB 1; Length 359;

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Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EDGIRIOPD 10
Db 8 EDGIRIOPD 17
RESULT 12
AC2R_MERUN
ID AC2R_MERUN STANDARD; PRT: 359 AA.
AC 035210.
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Type-1 angiotensin II receptor (AT1) (GAT1).
GN AGRI1.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxId=10047;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98434644; PubMed=9757050;
RA Moriuchi R., Shibata S., Himeno A., Johren O., Hoe K.L.,
RA Saavedra J.M.;
RT "Molecular cloning and pharmacological characterization of an atypical
RT gerbil angiotensin II type-1 receptor and its mRNA expression in brain
RT and peripheral tissues.";
RL Brain Res. Mol. Brain Res. 60:234-246(1998).
CC -1- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL: AF011903; AAB65429.1; -
DR HSSP: P34996; 1DDP.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOODPSN.
DR PROSITE: PS00237; G_PROTEIN_REC_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_REC_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
KW Palmitate; Phosphorylation.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 52 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 53 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 87 2 (POTENTIAL).
FT DOMAIN 88 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 142 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 143 162 4 (POTENTIAL).
FT DOMAIN 163 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 214 5 (POTENTIAL).
FT DOMAIN 215 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 241 262 6 (POTENTIAL).
FT DOMAIN 263 275 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 296 7 (POTENTIAL).
FT CARBOHYD 4 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT DISULFID 101 180 BY SIMILARITY.
FT LIPID 355 355 PALMITATE (POTENTIAL).
SQ SEQUENCE 359 AA: 40779 MW; 84C1EB9B6C4736DD CRC64;

Query Match
Best Local Similarity 100.0%; Score 9; DB 1; Length 359;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGIKRIODD 10
DB 9 DGIKRIODD 17

RESULT 13
AG2R_PIG STANDARD; PRT; 359 AA.
AC P30555;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Type-1 angiotensin II receptor (AT1).
GN AGT1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Arctic smooth muscle;
RX MEDLINE=93259232; PubMed=8491254;
RA Itazaki K., Shigeri Y., Fujimoto M.;
RT "Molecular cloning and characterization of the angiotensin receptor
  subtype in porcine aortic smooth muscle.";
RL Eur. J. Pharmacol. 245:147-156(1993).
CC -1- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
  ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
  CALCIN SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- PTM: CARBOXY-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL: D11340; BAA01952.1; -.
DR HSSP: P34966; 1DDO.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECPT_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
  Palmitate; Phosphorylation.
FT DOMAIN 1 27
FT TRANSMEM 28 52 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 53 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 87 2 (POTENTIAL).
FT DOMAIN 88 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 142 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 143 162 4 (POTENTIAL).
FT DOMAIN 163 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 214 5 (POTENTIAL).
FT DOMAIN 215 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 241 262 6 (POTENTIAL).
FT DOMAIN 263 275 7 (POTENTIAL).
FT TRANSMEM 276 296 7 (POTENTIAL).
FT DOMAIN 297 359 CYTOPLASMIC (POTENTIAL).

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FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 101 180 BY SIMILARITY.
FT LIPID 355 355 PALMITATE (POTENTIAL).
SQ SEQUENCE 359 AA: 40906 MW; D5B93968CC57ABF0 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 359;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 IKRIODD 10
DB 11 IKRIODD 17

RESULT 14
FLPA_METVO STANDARD; PRT; 228 AA.
ID FLPA_METVO
AC P35553;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrillarin-like pre-rRNA processing protein.
GN FLPA OR RPPA.
OS Methanococcus voltae.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanococcaceae; Methanococcus.
OX NCBI_TaxID=2188;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1537 / PS.
RX MEDLINE=94193565; PubMed=8144483;
RA Agha Amiri K.;
RT "Fibrillarin-like proteins occur in the domain Archaea.";
RL J. Bacteriol. 176:2124-2127(1994).
CC -1- FUNCTION: MAY BE INVOLVED IN PRE-RRNA PROCESSING.
CC -1- SIMILARITY: BELONGS TO THE FIBRILLARIN FAMILY.
CC -----
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CC -----
DR EMBL: X73988; CAA52166.1; -.
DR PIR: S34646; S34646.
DR HSSP: O58108; 1FBN.
DR InterPro: IPR000692; Fibrillarin.
DR Pfam: PF01269; Fibrillarin; 1.
DR PRINTS: PR00052; FIBRILLARIN.
DR PRODOM: PD004637; Fibrillarin.
DR PROSITE: PS00566; FIBRILLARIN; 1.
KW rRNA processing; RNA-binding.
SQ SEQUENCE 228 AA: 25618 MW; 0AB2418DE0E324CF CRC64;

Query Match
Best Local Similarity 100.0%; Score 6; DB 1; Length 228;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGIKRI 7
DB 18 DGIKRI 23

RESULT 15
HSLD_PSEAE STANDARD; PRT; 447 AA.
ID HSLD_PSEAE
AC Q9HUC5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)

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DT 15-JUN-2002 (rel. 41, last annotation update)
DE ATP-dependent hsl protease ATP-binding subunit hslU.
GN HSLU OR PA5054.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN
RM
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stoyer C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Gardner R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lardig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RA "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -! FUNCTION: Chaperone subunit of a proteasome-like degradation
CC complex (By similarity).
CC -! SUBUNIT: Interacts with hslV (By similarity).
CC -! SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -! SIMILARITY: BELONGS TO THE CLPX CHAPERONE FAMILY. HSLU SUBFAMILY.
CC
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CC -----
DR EMBL; AE004918; AAG08439.1; -.
DR HSSP; P32168; 1E94.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003959; AAA_ATPase_cent.
DR Pfam; PF00004; AAA; 1.
DR SMART; SM00382; AAA; 1.
DR TIGRFAMs; TIGR00390; hslU; 1.
DR Chaperone; ATP-binding; Complete proteome.
KW NP_BIND
FT 56
FT 63
SQ SEQUENCE 447 AA; 50082 MW; BEF52E52A4363043 CRC64;

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Query Match          60.0%; Score 6; DB 1; Length 447;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 EDGIKR 6
   |||||
DB 370 EDGIKR 375

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Search completed: November 12, 2002, 16:19:29
Job time : 12 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:15:53 ; Search time 15 Seconds
(without alignments)
19,615 Million cell updates/sec

Title: US-09-540-816-1
Perfect score: 52
Sequence: 1 EDGIRKRIQDD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	10	3	US-08-624-374-1
2	52	100.0	358	2	US-08-458-970A-11
3	52	100.0	359	1	US-08-041-219A-6
4	52	100.0	359	1	US-08-148-209A-4
5	52	100.0	359	1	US-08-417-1123-6
6	39	75.0	13	2	US-08-934-222-104
7	39	75.0	13	2	US-08-933-402-104
8	39	75.0	13	2	US-09-207-621-104
9	39	75.0	13	2	US-08-532-818-104
10	39	75.0	13	3	US-09-231-797-104
11	39	75.0	13	3	US-08-934-224-104
12	39	75.0	13	3	US-08-933-843-104
13	39	75.0	13	4	US-08-934-223-104
14	39	75.0	13	4	US-09-413-492-104
15	36	69.2	143	4	US-08-946-329A-52
16	35	67.3	455	5	PCR-US93-07261-13
17	35	67.3	1663	5	PCR-US93-07261-16
18	33	63.5	676	4	US-09-085-199B-7
19	33	63.5	1068	4	US-09-085-199B-11
20	33	63.5	2547	3	US-09-058-489-35
21	32	61.5	93	2	US-08-467-822-36
22	32	61.5	93	4	US-08-432-697-36
23	32	61.5	93	4	US-08-466-248-36
24	32	61.5	164	3	US-08-486-099-107
25	32	61.5	192	3	US-08-360-107A-117
26	32	61.5	192	3	US-08-484-223B-107
27	32	61.5	192	3	US-08-484-223B-107

28	32	61.5	192	3	US-08-919-597-107	Sequence 107, App
29	32	61.5	192	3	US-08-475-668A-107	Sequence 107, App
30	32	61.5	192	3	US-08-485-551A-107	Sequence 107, App
31	32	61.5	192	3	US-08-471-913A-107	Sequence 107, App
32	32	61.5	192	4	US-08-485-264A-107	Sequence 107, App
33	32	61.5	192	4	US-08-474-349A-107	Sequence 107, App
34	32	61.5	652	1	US-08-261-663A-6	Sequence 5, Appl1
35	32	61.5	652	4	US-09-357-206A-5	Sequence 5, Appl1
36	32	61.5	652	5	PCT-US95-07554A-6	Sequence 6, Appl1
37	32	61.5	983	4	US-09-412-554A-2	Sequence 2, Appl1
38	32	61.5	1143	2	US-08-310-912A-108	Sequence 108, App
39	32	61.5	1143	4	US-09-301-085-108	Sequence 108, App
40	32	61.5	1143	5	PCT-US95-04589-108	Sequence 108, App
41	32	61.5	1144	1	US-08-261-663A-4	Sequence 2, Appl1
42	32	61.5	1144	1	US-08-261-663A-4	Sequence 4, Appl1
43	32	61.5	1144	3	US-08-930-996A-9	Sequence 9, Appl1
44	32	61.5	1144	4	US-09-357-206A-3	Sequence 3, Appl1
45	32	61.5	1144	5	PCT-US95-07754A-2	Sequence 2, Appl1

ALIGNMENTS

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RESULT 1
US-08-624-374-1
; Sequence 1, Application US/08624374
; Patent No. 6063620
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: NOVEL HYBRIDOMA & MONOCLONAL
; NUMBER OF INVENTION: ANTIBODIES PRODUCED THEREBY
; NUMBER OF SEQUENCES: 1
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; OPERATING SYSTEM: DOS 6.2/Windows 3.1
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/624,374
; FILING DATE: March 27, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB94/02100
; FILING DATE: 27-SEPT-1994
; APPLICATION NUMBER: GB 9319877.8
; FILING DATE: 27-SEPT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Klein, Richard M.
; REGISTRATION NUMBER: 33,000
; REFERENCE/DOCKET NUMBER: BKY 2 040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (216) 861-5582
; TELEFAX: (216) 241-1666
; TELEX: (216) 980162
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; CELL LINE: Hybridoma
; US-08-624-374-1

Query Match          100.0%; Score 52; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00085;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 EDGIRKRIQDD 10
DB 1 EDGIRKRIQDD 10

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RESULT 2
US-08-458-970A-11
; Sequence 11, Application US/08458970A
; Patent No. 5861272
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: C5a Receptor
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458, 970A
; FILING DATE: June 2, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09234
; FILING DATE: 16 AUG. 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-458-970A-11
;
Query Match 100.0%; Score 52; DB 2; Length 358;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0
;
QY 1 EDGIRKIODD 10
; |||||
;
Db 7 EDGIRKIODD 16
;
RESULT 3
US-08-041-219A-6
; Sequence 6, Application US/08041219A
; Patent No. 5427922
; GENERAL INFORMATION:
; APPLICANT: FUJISAMA, YUKIO
; APPLICANT: KURODA, SHUN'ICHI
; APPLICANT: KONISHI, HIROAKI
; TITLE OF INVENTION: ANGIOTENSIN II TYPE-1 RECEPTOR AND ITS
; TITLE OF INVENTION: PRODUCTION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEGNER, CANTOR, MUELLER & PLAYER
; STREET: 1233 20th Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036
; COMPUTER READABLE FORM:

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MEDIMUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/041,219A
FILING DATE: 31-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 085445-1992
FILING DATE: 07-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 101393-1992
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 027835-1993
FILING DATE: 17-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Douglas P.
REGISTRATION NUMBER: 30,300
REFERENCE/DOCKET NUMBER: P-8700-23781
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-0400
TELEFAX: (202) 835-0605
TELEX: 440706
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Placental
US-08-041-219A-6

Query Match      100.0%: Score 52; DB 1; Length 359;
Best Local Similarity 100.0%: Pred. NO. 0.044,
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 EDGIRKIODD 10
        |||||||||
Db      8 EDGIRKIODD 17

RESULT 4
US-08-148-209A-4
; Sequence 4, Application US/08148209A
; Patent No. 5556780
; GENERAL INFORMATION:
; APPLICANT: Dzau, Victor J
; APPLICANT: Mukoyama, Masashi
; TITLE OF INVENTION: TYPE-2 ANGIOTENSIN II RECEPTOR AND GENE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/148, 209A
; FILING DATE: 05-NOV-1993
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
;

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REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-58491-1/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-148-209A-4

Query Match 100.0%; Score 52; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGIKRIODD 10
|
8 EDGIKRIODD 17

RESULT 5
US-08-417-122-6
Sequence 6, Application US/08417122
Patent No. 5595882
GENERAL INFORMATION:
APPLICANT: FUJISAWA, Yukio
APPLICANT: KURODA, Shun'ichi
APPLICANT: KONISHI, Hiroaki
TITLE OF INVENTION: ANGIOGENSIN II TYPE-1 RECEPTOR AND ITS
TITLE OF INVENTION: PRODUCTION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEGNER, CANTOR, MUELLER & PLAYER
STREET: 1233 20th Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,122
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/041,219
FILING DATE: 31-MAR-1993
APPLICATION NUMBER: JP 085445-1992
FILING DATE: 07-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 101393-1992
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 027835-1993
FILING DATE: 17-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Douglas P.
REGISTRATION NUMBER: 30,300
REFERENCE/DOCKET NUMBER: P-87/00-23781
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-0400
TELEFAX: (202) 835-0605
TELEX: 440706
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Placental
US-08-417-122-6

Query Match 100.0%; Score 52; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGIKRIODD 10
|
8 EDGIKRIODD 17

RESULT 6
US-08-934-222-104
Sequence 104, Application US/08934222
Patent No. 5928896
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interacti-
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,222
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-934-222-104

Query Match 75.0%; Score 39; DB 2; Length 13;
Best Local Similarity 88.9%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DGIKRIODD 10
|
1 DGIKRIODD 9

RESULT 7
US-08-933-402-104
; Sequence 104, Application US/08933402
; Patent No. 5948887
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,402
; FILING DATE: 19-SEPT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-933-402-104
Query Match 75.0%; Score 39; DB 2; Length 13;
Best Local Similarity 88.9%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 DGIKRIODD 10
DB 1 DGIKRIODD 9
RESULT 8
US-09-207-621-104
; Sequence 104, Application US/09207621
; Patent No. 5952465
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction S
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/207,621
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-207-621-104
Query Match 75.0%; Score 39; DB 2; Length 13;
Best Local Similarity 88.9%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 DGIKRIODD 10
DB 1 DGIKRIODD 9
RESULT 9
US-08-532-818-104
; Sequence 104, Application US/08532818
; Patent No. 5965698
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interacti
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993

ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-532-818-104

Query Match 75.0%; Score 39; DB 2; Length 13;
Best Local Similarity 88.9%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DGIKRIQDD 10
DB 1 DPKIRIQDD 9

RESULT 10
US-09-231-797-104
Sequence 104, Application US/09231797
Patent No. 6084066
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Plank A Protein-Protein Interaction
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,797
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-231-797-104

Query Match 75.0%; Score 39; DB 3; Length 13;
Best Local Similarity 88.9%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 DGIKRIQDD 10
DB 1 DPKIRIQDD 9

DB 1 DPKIRIQDD 9

RESULT 11
US-08-934-224-104
Sequence 104, Application US/08934224
Patent No. 6100044
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha

TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Plank A Protein-Protein Interacti
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,224
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996

APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.

REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-934-224-104

Query Match 75.0%; Score 39; DB 3; Length 13;
Best Local Similarity 88.9%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DGIKRIQDD 10
DB 1 DPKIRIQDD 9

RESULT 12
US-08-933-843-104
Sequence 104, Application US/08933843
Patent No. 6111069
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.

APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Plank A Protein-Protein Interacti
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner

STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,843
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-933-843-104

Query Match 75.0%; Score 39; DB 3; Length 13;
Best Local Similarity 88.9%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DGIKRIQDD 10
| | | | | | | |
Db 1 DGIKRIQDD 9

RESULT 13
US-08-934-223-104
Sequence 104, Application US/08934223
Patent No. 6147189
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,223
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-934-223-104

Query Match 75.0%; Score 39; DB 4; Length 13;
Best Local Similarity 88.9%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DGIKRIQDD 10
| | | | | | | |
Db 1 DGIKRIQDD 9

RESULT 14
US-09-413-492-104
Sequence 104, Application US/09413492
Patent No. 6258550
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interacti
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/413,492
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-413-492-104

Query Match 75.0%; Score 39; DB 4; Length 13;
 Best Local Similarity 88.9%; Pred. No. 0.28;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DGKRIODD 10
 | | | | | | | |
 Db 1 DPKRIODD 9

RESULT 15

US-08-946-329A-52
 ; Sequence 52, Application US/08946329A
 ; Patent No. 6057091

GENERAL INFORMATION:

APPLICANT: Beachy, Philip A.
 APPLICANT: Porter, Jeffrey A.

TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES

NUMBER OF SEQUENCES: 109

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/946,329A

FILING DATE: 07-OCT-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/061,323

FILING DATE: 07-OCT-1996

APPLICATION NUMBER: 08/729,743

FILING DATE: 10-JUL-1996

APPLICATION NUMBER: 08/567,357

FILING DATE: 04-DEC-1995

APPLICATION NUMBER: 08/349,498

FILING DATE: 02-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Lisa A.

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07265/140001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERISTICS:

LENGTH: 143 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-946-329A-52

Query Match 69.2%; Score 36; DB 3; Length 143;
 Best Local Similarity 77.8%; Pred. No. 14;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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 | | | | | | | |
 Db 11 EDGIRKIKD 19

Search completed: November 12, 2002, 16:18:13
 Job time : 16 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:16:38 ; Search time 10 seconds
(without alignments)
14,419 Million cell updates/sec

Title: US-09-540-816-1
Perfect score: 52
Sequence: 1 EDGKIRIQQD 10

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Gapop 10.0 , Gapext 0.5

Searched: 92612 seqs, 14418503 residues

Total number of hits satisfying chosen parameters: 92612

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEM_PUB pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCr_NEM_PUB pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEM_PUB pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep:*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep:*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEM_PUB pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep:*
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- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	359	10 US-09-867-569-9	Sequence 9, Appl
2	52	100.0	359	10 US-09-966-871-81	Sequence 81, Appl
3	52	100.0	359	12 US-10-039-645-81	Sequence 81, Appl
4	36	66.2	145	10 US-09-867-550-66	Sequence 66, Appl
5	36	66.2	417	9 US-09-879-959-2	Sequence 2, Appl
6	35	67.3	71	10 US-09-815-242-4926	Sequence 4926, A
7	35	67.3	75	10 US-09-815-242-10918	Sequence 10918, A
8	35	67.3	352	10 US-09-925-299-963	Sequence 963, Appl
9	35	67.3	1884	10 US-09-785-770A-17	Sequence 17, Appl
10	35	67.3	1907	10 US-09-785-770A-16	Sequence 16, Appl
11	33	65.5	232	9 US-09-792-251-8	Sequence 8, Appl
12	33	65.5	179	10 US-09-815-242-12256	Sequence 12256, A
13	32	61.5	388	10 US-09-815-242-5250	Sequence 5250, Ap
14	32	61.5	559	10 US-09-815-242-11904	Sequence 11904, A
15	32	61.5	652	10 US-09-813-742-5	Sequence 5, Appl
16	32	61.5	773	9 US-09-808-602-60	Sequence 60, Appl
17	32	61.5	850	9 US-09-808-602-58	Sequence 58, Appl
18	32	61.5	879	9 US-10-108-605-217	Sequence 217, Appl
19	32	61.5	983	9 US-09-808-602-73	Sequence 73, Appl

20	32	61.5	1143	10 US-09-867-852-108	Sequence 108, App
21	32	61.5	1144	10 US-09-813-742-3	Sequence 3, Appl
22	32	61.5	1192	10 US-09-815-242-10903	Sequence 10903, A
23	32	61.5	2076	10 US-09-815-242-5815	Sequence 5815, Ap
24	32	61.5	2186	10 US-09-815-242-12913	Sequence 12913, A
25	31	59.6	132	10 US-09-867-550-60	Sequence 60, Appl
26	31	59.6	179	10 US-09-780-717-32	Sequence 32, Appl
27	31	59.6	179	10 US-09-780-717-35	Sequence 35, Appl
28	31	59.6	342	10 US-09-815-242-10958	Sequence 10958, A
29	31	59.6	932	10 US-09-788-657-17	Sequence 17, Appl
30	31	59.6	932	10 US-09-788-657-18	Sequence 18, Appl
31	30	57.7	37	10 US-09-864-761-47077	Sequence 47077, A
32	30	57.7	50	10 US-09-867-550-1266	Sequence 1266, Ap
33	30	57.7	60	10 US-09-867-550-978	Sequence 978, App
34	30	57.7	69	10 US-09-864-761-45962	Sequence 45962, A
35	30	57.7	180	10 US-09-765-272-186	Sequence 186, App
36	30	57.7	204	10 US-09-815-242-13428	Sequence 13428, A
37	30	57.7	204	10 US-09-815-242-13687	Sequence 13687, A
38	30	57.7	247	10 US-09-815-242-13461	Sequence 13461, A
39	30	57.7	247	10 US-09-815-242-13622	Sequence 13622, A
40	30	57.7	249	10 US-09-903-410-39	Sequence 39, Appl
41	30	57.7	266	9 US-09-981-353-141	Sequence 141, App
42	30	57.7	266	10 US-09-935-390A-29	Sequence 29, Appl
43	30	57.7	266	10 US-09-935-390A-38	Sequence 38, Appl
44	30	57.7	266	10 US-09-919-172-51	Sequence 51, Appl
45	30	57.7	302	10 US-09-815-242-5495	Sequence 5495, Ap

ALIGNMENTS

RESULT 1
US-09-867-569-9
; Sequence 9, Application US/09867569
; Patent No. US2001003650A1
; GENERAL INFORMATION:
; APPLICANT: Li et al.
; TITLE OF INVENTION: C5a Receptor
; FILE REFERENCE: PFI30DCL
; CURRENT FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 09/082,529
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: 08/458,970
; PRIOR FILING DATE: 1995-05-02
; PRIOR APPLICATION NUMBER: PCT/US94/09234
; PRIOR FILING DATE: 1994-08-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-867-569-9

Query Match 100.0% Score 52; DB 10; Length 359;
Best Local Similarity 100.0% Pred. NO. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGKIRIQQD 10
|||||||
DB 8 EDGKIRIQQD 17

RESULT 2
US-09-966-871-81
; Sequence 81, Application US/09966871
; Patent No. US20020127539A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; TITLE OF INVENTION: Assays for Identifying Receptors Having
; TITLE OF INVENTION: Alterations in Signaling
; FILE REFERENCE: 00398/512002

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; CURRENT APPLICATION NUMBER: US/09/966,871
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,302
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/288,644
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-871-81

Query Match
Best Local Similarity 100.0%; Score 52; DB 10; Length 359;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGIRKRIODD 10
Db 8 EDGIRKRIODD 17

RESULT 3
US-10-039-645-81
; Sequence 81, Application US/10039645
; Patent No. US20020147170A1
; GENERAL INFORMATION:
; APPLICANT: Koplin, Alan S.
; APPLICANT: Beinborn, Martin
; TITLE OF INVENTION: Constitutively Active, Hypersensitive,
; FILE REFERENCE: 00398/510002
; CURRENT APPLICATION NUMBER: US/10/039,645
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/243,550
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-645-81

Query Match
Best Local Similarity 100.0%; Score 52; DB 12; Length 359;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGIRKRIODD 10
Db 8 EDGIRKRIODD 17

RESULT 4
US-09-867-550-66
; Sequence 66, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehrahan, Fuad,
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: No. US20020082206A1 Polynucleotides from Atherogenic Cells and
; FILE REFERENCE: 21402-013 (Cura-313)
; CURRENT APPLICATION NUMBER: US/09/867,550
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: USSN 60/208,427
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2125
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 66
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-867-550-66

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Best Local Similarity 69.2%; Score 36; DB 10; Length 145;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDGIRKRIODD 10
Db 98 EDGIRKRIODD 107

RESULT 5
US-09-879-959-2
; Sequence 2, Application US/09879959
; Patent No. US20020160489A1
; GENERAL INFORMATION:
; APPLICANT: Weigel, Paul H
; APPLICANT: Kumari, Kashama
; APPLICANT: DeAngelis, Paul
; TITLE OF INVENTION: STREPTOCOCCUS EQUISIMILIS HYALURONAN SYNTHASE GENE AND EXPRESS
; FILE REFERENCE: 3554.049
; CURRENT APPLICATION NUMBER: US/09/879,959
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 09/469,200
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 09/178,851
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
US-09-879-959-2

Query Match
Best Local Similarity 69.2%; Score 36; DB 9; Length 417;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDGIRKRIODD 9
Db 108 EDGIRKRIODD 116

RESULT 6
US-09-815-242-4926
; Sequence 4926, Application US/09815242
; Patent No. US2002061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trivick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
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; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4926
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-4926
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Query Match          67.3%; Score 35; DB 10; Length 71;
Best Local Similarity 66.7%; Pred. No. 3.2;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 1 EDGIRRIOD 9
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Db 53 EDGIQTVD 61
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RESULT 7
US-09-815-242-10918

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; Sequence 10918, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10918
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10918
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Query Match          67.3%; Score 35; DB 10; Length 75;
Best Local Similarity 66.7%; Pred. No. 3.3;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 1 EDGIRRIOD 9
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Db 56 EDGIQTVD 64
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RESULT 8
US-09-925-299-963
; Sequence 963, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 963
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (281)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-963
```

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Query Match          67.3%; Score 35; DB 10; Length 352;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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QY 1 EDGIRRIODD 10
    ||:|:|
Db 142 EDQVKLEDD 151
```

```
RESULT 9
US-09-785-770A-17
; Sequence 17, Application US/09785770A
; Patent No. US20020103360A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Barnes, Thomas M.
; TITLE OF INVENTION: A NOVEL PROTEIN RELATED TO MELANOMA-INHIBITING PROTEIN
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334-328001
; CURRENT APPLICATION NUMBER: US/09/785,770A
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/387,462
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: US 09/145,056
; PRIOR FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 4.0
; SEQ ID NO 17
; LENGTH: 1864
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-785-770A-17
```

```
Query Match          67.3%; Score 35; DB 10; Length 1864;
Best Local Similarity 50.0%; Pred. No. 11e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 EDGIRRIODD 10
    ||:|:|
Db 1466 EDQVKLEDD 1475
```

```
RESULT 10
US-09-785-770A-16
; Sequence 16, Application US/09785770A
; Patent No. US20020103360A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Barnes, Thomas M.
; TITLE OF INVENTION: A NOVEL PROTEIN RELATED TO MELANOMA-INHIBITING PROTEIN
; FILE REFERENCE: 07334-328001
; CURRENT APPLICATION NUMBER: US/09/785,770A
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/387,462
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: US 09/145,056
; PRIOR FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 4.0
; SEQ ID NO 16
; LENGTH: 1907
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-785-770A-16
```

```
Query Match          67.3%; Score 35; DB 10; Length 1907;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 EDGIRKRIQDD 10
      11 :||::||
Db      1489 EDQVKRLIEDD 1498
```

```
RESULT 11
US-09-792-251-8
; Sequence 8, Application US/09792251
; Patent No. US20020160364A1
; GENERAL INFORMATION:
; APPLICANT: Fritze, Christian
; APPLICANT: Youngman, Philip
; APPLICANT: Guzman, Luz-Maria
; TITLE OF INVENTION: USE OF YACM AND YQET, ESSENTIAL BACTERIAL GENES AND POLYPEPTIDES
; FILE REFERENCE: 06286-140001
; CURRENT APPLICATION NUMBER: US/09/792,251
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-792-251-8
```

```
Query Match          63.5%; Score 33; DB 9; Length 232;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 EDGIRKRIQD 9
      11 :|||:|
Db      135 KDTIKRVQD 143
```

```
RESULT 12
US-09-815-242-12256
; Sequence 12256, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
```

```
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12256
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12256
```

```
Query Match          61.5%; Score 32; DB 10; Length 179;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 EDGIRKRIQD 9
      11 :|||:|
Db      75 DDEIKRIED 83
```

```
RESULT 13
US-09-815-242-5250
; Sequence 5250, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5250
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
```

US-09-815-242-5250

Query Match

61.5%: Score 32; DB 10; Length 388;
Best Local Similarity 66.7%: Pred. No. 72;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDGIRI0DD 9

DB 71 DDEIKRIED 79

RESULT 14

US-09-815-242-11904

; Sequence 11904, Application US/09815242
; Patent No. US20020061569A1

GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Karl L.

; APPLICANT: Zyskind, Judith W.

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John D.

; APPLICANT: Carr, Grant J.

; APPLICANT: Yamamoto, Robert T.

; TITLE OF INVENTION: Identification of Essential Genes in

; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO: 11904

; LENGTH: 559

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-815-242-11904

Query Match

61.5%: Score 32; DB 10; Length 559;
Best Local Similarity 62.5%: Pred. No. 11e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 GIKRI0DD 10

DB 432 GIKOLEDD 439

RESULT 15

US-09-813-742-5

; Sequence 5, Application US/09813742

; Patent No. US20020004944A1

GENERAL INFORMATION:

; APPLICANT: Baker, Barbara

; APPLICANT: Dinesh-Kumar, S.P.

; TITLE OF INVENTION: NON-PATHOGEN INDUCED SYSTEMIC ACQUIRED RESISTANCE (SAR) IN PLANTS

; FILE REFERENCE: 042250/209601 (5830-12)

; CURRENT APPLICATION NUMBER: US/09/813,742

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,027

; PRIOR FILING DATE: 2000-03-21

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 5

; LENGTH: 652

; TYPE: PRT

; ORGANISM: Nicotiana glauca

US-09-813-742-5

Query Match

61.5%: Score 32; DB 10; Length 652;
Best Local Similarity 60.0%: Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDGIRI0DD 10

DB 37 DGIKIF0DD 46

Search completed: November 12, 2002, 16:18:29
Job time : 10 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:16:53 ; Search time 35 Seconds
(without alignments)
38.072 Million cell updates/sec

Title: US-09-540-816-1

Perfect score: 10

Sequence: 1 EDGIKRIQDD 10

Seeding (kappa, omega, gapop)
Gapop 60.0, Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size: 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

A.Geneseq_101002:*

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4: /SIDs2/gcgdata/geneseq/genesqp-emb1/AA1983.DAT:*
5: /SIDs2/gcgdata/geneseq/genesqp-emb1/AA1984.DAT:*
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9: /SIDs2/gcgdata/geneseq/genesqp-emb1/AA1988.DAT:*
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11: /SIDs2/gcgdata/geneseq/genesqp-emb1/AA1990.DAT:*
12: /SIDs2/gcgdata/geneseq/genesqp-emb1/AA1991.DAT:*
13: /SIDs2/gcgdata/geneseq/genesqp-emb1/AA1992.DAT:*
14: /SIDs2/gcgdata/geneseq/genesqp-emb1/AA1993.DAT:*
15: /SIDs2/gcgdata/geneseq/genesqp-emb1/AA1994.DAT:*
16: /SIDs2/gcgdata/geneseq/genesqp-emb1/AA1995.DAT:*
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18: /SIDs2/gcgdata/geneseq/genesqp-emb1/AA1997.DAT:*
19: /SIDs2/gcgdata/geneseq/genesqp-emb1/AA1998.DAT:*
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21: /SIDs2/gcgdata/geneseq/genesqp-emb1/AA2000.DAT:*
22: /SIDs2/gcgdata/geneseq/genesqp-emb1/AA2001.DAT:*
23: /SIDs2/gcgdata/geneseq/genesqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	100.0	10	16	AA72230
2	10	100.0	15	15	AA74531
3	10	100.0	359	21	AA802844
4	10	100.0	359	21	AA802848
5	10	100.0	359	21	AA802849
6	10	100.0	359	21	AA802850
7	10	100.0	359	23	AA020951
8	10	100.0	359	23	AAU78654
9	10	100.0	359	23	AAU78655
10	10	100.0	359	23	AAU78656

11	10	100.0	360	21	AA802851
12	7	70.0	13	15	AA67111
13	6	60.0	62	21	AA611661
14	6	60.0	440	19	AAW25782
15	6	60.0	440	22	ABB65401
16	6	60.0	509	22	ABB60875
17	6	60.0	586	15	AA849579
18	6	60.0	656	22	ABB65787
19	6	60.0	1085	12	AA811604
20	5	50.0	7	22	AAW46059
21	5	50.0	7	22	AAW46064
22	5	50.0	7	22	AAW46069
23	5	50.0	10	22	AAW46449
24	5	50.0	10	22	AAW46449
25	5	50.0	10	22	AAW46449
26	5	50.0	11	21	AAW46449
27	5	50.0	14	22	AAW46449
28	5	50.0	14	22	AAW46449
29	5	50.0	16	14	AAW42185
30	5	50.0	20	12	AAW42185
31	5	50.0	22	12	AAW42185
32	5	50.0	22	12	AAW42185
33	5	50.0	25	12	AAW42185
34	5	50.0	25	12	AAW42185
35	5	50.0	30	9	AAW42185
36	5	50.0	40	12	AAW42185
37	5	50.0	45	19	AAW42185
38	5	50.0	48	11	AAW42185
39	5	50.0	50	22	AAW42185
40	5	50.0	50	22	AAW42185
41	5	50.0	53	22	AAW42185
42	5	50.0	57	10	AAW42185
43	5	50.0	59	19	AAW42185
44	5	50.0	60	9	AAW42185
45	5	50.0	60	12	AAW42185

ALIGNMENTS

RESULT 1
AA72230
AA72230 standard; Peptide: 10 AA.

AA72230;
01-DEC-1995 (first entry)

Epitope of rat vascular smooth muscle ATI receptor (residues 8-17).

Monoclonal antibody; ATI receptor; subtype: Angiotensin II receptor;
rat vascular smooth muscle; conserved; mammalian ATI receptor;
detection; cancer diagnosis; sperm motility; contraception.

Synthetic.
WO9509186-A.

06-APR-1995.
27-SEP-1994; 94WO-GB02100.
27-SEP-1993; 93GB-0019877.

(QUEEN) QUEEN MARY & WESTFIELD COLLEGE.
Barker S, Vinson GP;
WPI: 1995-147395/19.
Monoclonal antibody to ATI angiotensin receptor - used for
detection and control of uterine contractions and
vasoconstriction e.g. for treating hypertension

```
XX Claim 3; Page 13; 24pp; English.
XX
XX Monoclonal antibodies (Mabs) that bind to the AT1 receptor (a
CC subtype of Angiotensin II receptor) are claimed. The Abs
CC specifically bind to amino acid residues 8 to 17 of the rat vascular
CC smooth muscle AT1 receptor. This sequence is conserved in all
CC mammalian AT1 receptors so far cloned. The Mabs can be used for
CC detection of AT1 receptors, e.g. in cancer diagnosis. They can also
CC be used to study and measure sperm motility and can be used in
CC contraception.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 10; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGIKRIQDD 10
   |||||
   1 EDGIKRIQDD 10
DB 1 EDGIKRIQDD 10

RESULT 2
AAR44531
ID AAR44531 standard; Protein; 359 AA.
XX
AC AAR44531;
XX
XX 24-JUN-1994 (first entry)
XX
DE Human angiotensin II type 1 receptor.
XX
XX Angiotensin; Ang II; receptor; antagonist; hypertension.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH 187..313
FT Protein /note="claim 1"
FT
XX
XX CA2093495-A.
XX
XX 08-OCT-1993.
XX
XX 06-APR-1993; 93CA-2093495.
XX
XX 07-APR-1992; 92JP-0085445.
XX
XX 21-APR-1992; 92JP-0101393.
XX
XX 17-FEB-1993; 93JP-0027835.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Fujisawa Y, Konishi H, Kuroda S;
XX
XX WPI; 1994-000128/01.
XX
XX N-PSDB; AAQ53486.
XX
XX Human angiotensin II type 1 receptor polypeptide - useful for
XX determining human angiotensin II type 1 receptor antagonist
XX activity
XX
XX Claim 2; Fig 1; 42pp; English.
XX
XX Human Ang II type 1 receptor is useful for determining the
XX bioactivity of angiotensin II type 1 receptor antagonists which are
XX useful for treating hypertension. The Ang II type 1 receptor gene
XX was derived from human placenta and is contained in plasmid
XX PHAHP116.
XX
SQ Sequence 359 AA;

Query Match 100.0%; Score 10; DB 15; Length 359;
```

```
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGIKRIQDD 10
   |||||
   8 EDGIKRIQDD 17
DB 8 EDGIKRIQDD 17

RESULT 3
AAB02844
ID AAB02844 standard; Protein; 359 AA.
XX
AC AAB02844;
XX
XX 22-AUG-2000 (first entry)
XX
DE Human G protein coupled receptor AT1 protein SEQ ID NO:66.
XX
XX Human; G protein coupled receptor; GPCR; transmembrane receptor;
XX identification; agonist; screening; therapeutic; pharmaceutical;
XX mutant.
XX
XX Homo sapiens.
XX
XX WO200022131-A2.
XX
XX 20-APR-2000.
XX
XX 13-OCT-1999; 99WO-US24065.
XX
XX 13-OCT-1998; 98US-0170496.
XX
XX 12-NOV-1998; 98US-0108029.
XX
XX 20-NOV-1998; 98US-0109213.
XX
XX 27-NOV-1998; 98US-0110060.
XX
XX 16-FEB-1999; 99US-0120416.
XX
XX 26-FEB-1999; 99US-0121852.
XX
XX 12-MAR-1999; 99US-0123944.
XX
XX 12-MAR-1999; 99US-0123945.
XX
XX 12-MAR-1999; 99US-0123946.
XX
XX 12-MAR-1999; 99US-0123948.
XX
XX 12-MAR-1999; 99US-0123949.
XX
XX 12-MAR-1999; 99US-0123951.
XX
XX 28-MAY-1999; 99US-0136436.
XX
XX 28-MAY-1999; 99US-0136437.
XX
XX 28-MAY-1999; 99US-0136439.
XX
XX 28-MAY-1999; 99US-0137127.
XX
XX 28-MAY-1999; 99US-0137131.
XX
XX 28-MAY-1999; 99US-0137567.
XX
XX 30-JUN-1999; 99US-0141448.
XX
XX 27-AUG-1999; 99US-0151114.
XX
XX 03-SEP-1999; 99US-0152524.
XX
XX 29-SEP-1999; 99US-0156633.
XX
XX 29-SEP-1999; 99US-0156553.
XX
XX 29-SEP-1999; 99US-0156634.
XX
XX
XX (AREN-) ARENA PHARM INC.
XX
XX Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;
XX Gore M, Liaw CW, Lin I, Lowitz K, White C;
XX
XX WPI; 2000-317986/27.
XX
XX N-PSDB; AAA46062.
XX
XX Non-endogenous, human G protein-coupled receptors for screening
XX receptor, inverse or partial agonists useful as therapeutic agents -
XX
XX Example 1; Page 129-130; 187pp; English.
XX
XX The present invention describes transmembrane receptors, preferably
XX human G protein coupled receptors (GPCR), for which the endogenous
XX ligand is unknown (orphan GPCR receptors). More specifically the present
XX invention relates to non-endogenous, constitutively activated versions
XX of a human GPCR. These non-endogenous human GPCRs can be useful for
```

CC the direct identification of candidate compounds as receptors agonists,
CC inverse agonists or partial agonists for use as pharmaceutical agents.
CC AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
CC the exemplification of the present invention.

XX SQ Sequence 359 AA;

Query Match 100.0%; Score 10; DB 21; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGIRRIODD 10
|||||
DB 8 EDGIRRIODD 17

RESULT 4
AAB02848
ID AAB02848 standard; Protein: 359 AA.

XX AC AAB02848;

DT 22-AUG-2000 (first entry)

XX DE Human G protein coupled receptor hA11 F239K protein SEQ ID NO:90.

XX KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
XX identification; agonist; screening; therapeutic; pharmaceutical;
XX mutant.

OS Homo sapiens.
OS Synthetic.

XX PN WO200022131-A2.

XX PD 20-APR-2000.

XX PF 13-OCT-1999; 99WO-US24065.

XX PR 13-OCT-1998; 98US-0170496.

XX PR 12-NOV-1998; 98US-0108029.

XX PR 20-NOV-1998; 98US-0109213.

XX PR 27-NOV-1998; 98US-0110060.

XX PR 16-FEB-1999; 99US-0120416.

XX PR 26-FEB-1999; 99US-0121852.

XX PR 12-MAR-1999; 99US-0123944.

XX PR 12-MAR-1999; 99US-0123945.

XX PR 12-MAR-1999; 99US-0123946.

XX PR 12-MAR-1999; 99US-0123949.

XX PR 12-MAR-1999; 99US-0123951.

XX PR 28-MAY-1999; 99US-0136436.

XX PR 28-MAY-1999; 99US-0136437.

XX PR 28-MAY-1999; 99US-0136439.

XX PR 28-MAY-1999; 99US-0137127.

XX PR 28-MAY-1999; 99US-0137131.

XX PR 28-MAY-1999; 99US-0137567.

XX PR 30-JUN-1999; 99US-0141448.

XX PR 27-AUG-1999; 99US-0151114.

XX PR 03-SEP-1999; 99US-0152524.

XX PR 29-SEP-1999; 99US-0156633.

XX PR 29-SEP-1999; 99US-0156555.

XX PR 29-SEP-1999; 99US-0156634.

XX PA (AREN-) ARENA PHARM INC.

XX PI Behan DP, Lehmann-Brulisma K, Chalmers DF, Chen R, Dang HT;

XX PI Gore M, Liaw CW, Lin I, Lowitz K, White C;

XX DR WPT; 2000-317986/27.

XX DR N-PSDB; AAA46082.

XX PT Non-endogenous, human G protein-coupled receptors for screening

PT receptor, inverse or partial agonists useful as therapeutic agents
XX
XX Example 2: Page 143-144; 187pp; English.

XX CC The present invention describes transmembrane receptors, preferably
XX human G protein coupled receptors (GPCR), for which the endogenous
XX ligand is unknown (Orphan GPCR receptors). More specifically the present
XX invention relates to non-endogenous, constitutively activated versions
XX of a human GPCR. These non-endogenous human GPCRs can be useful for
XX the direct identification of candidate compounds as receptors agonists,
XX inverse agonists or partial agonists for use as pharmaceutical agents.
XX AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
XX the exemplification of the present invention.

XX SQ Sequence 359 AA;

Query Match 100.0%; Score 10; DB 21; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGIRRIODD 10
|||||
DB 8 EDGIRRIODD 17

RESULT 5
AAB02849
ID AAB02849 standard; Protein: 359 AA.

XX AC AAB02849;

DT 22-AUG-2000 (first entry)

XX DE Human G protein coupled receptor hA11 mutant protein SEQ ID NO:94.

XX KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
XX identification; agonist; screening; therapeutic; pharmaceutical;
XX mutant.

OS Homo sapiens.
OS Synthetic.

XX PN WO200022131-A2.

XX PD 20-APR-2000.

XX PF 13-OCT-1999; 99WO-US24065.

XX PR 13-OCT-1998; 98US-0170496.

XX PR 12-NOV-1998; 98US-0108029.

XX PR 20-NOV-1998; 98US-0109213.

XX PR 27-NOV-1998; 98US-0110060.

XX PR 16-FEB-1999; 99US-0120416.

XX PR 26-FEB-1999; 99US-0121852.

XX PR 12-MAR-1999; 99US-0123944.

XX PR 12-MAR-1999; 99US-0123945.

XX PR 12-MAR-1999; 99US-0123946.

XX PR 12-MAR-1999; 99US-0123949.

XX PR 12-MAR-1999; 99US-0123951.

XX PR 28-MAY-1999; 99US-0136436.

XX PR 28-MAY-1999; 99US-0136437.

XX PR 28-MAY-1999; 99US-0136439.

XX PR 28-MAY-1999; 99US-0137127.

XX PR 28-MAY-1999; 99US-0137567.

XX PR 30-JUN-1999; 99US-0141448.

XX PR 27-AUG-1999; 99US-0151114.

XX PR 03-SEP-1999; 99US-0152524.

XX PR 29-SEP-1999; 99US-0156633.

XX PR 29-SEP-1999; 99US-0156555.

XX PR 29-SEP-1999; 99US-0156634.

```

PA (AREN-) ARENA PHARM INC.
XX Behan DP, Lehmann-Brusma K, Chalmers DT, Chen R, Dang HT;
PI Gore M, Liaw CW, Lin I, Lowitz K, White C;
XX WPI: 2000-317986/27.
DR N-PSDB; AAA46084.
XX
PT Non-endogenous, human G protein-coupled receptors for screening
PT receptor, inverse or partial agonists useful as therapeutic agents
XX
PS Example 2; Page 146-147; 187pp; English.
XX
CC The present invention describes transmembrane receptors, preferably
CC human G protein coupled receptors (GPCR), for which the endogenous
CC ligand is unknown (orphan GPCR receptors). More specifically the present
CC invention relates to non-endogenous, constitutively activated versions
CC of a human GPCR. These non-endogenous human GPCRs can be useful for
CC the direct identification of candidate compounds as receptors agonists,
CC inverse agonists or partial agonists for use as pharmaceutical agents.
CC AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
CC the exemplification of the present invention.
XX
SQ Sequence 359 AA;
Query Match 100.0%; Score 10; DB 21; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EDGIRKRIQDD 10
DB 8 EDGIRKRIQDD 17
XX
RESULT 6
AAB02850
ID AAB02850 standard; Protein; 359 AA.
XX
AC AAB02850;
XX
DT 22-AUG-2000 (first entry)
XX
DE Human G protein coupled receptor hAT1 mutant; protein SEQ ID NO:100.
XX
KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
KW identification; agonist; screening; therapeutic; pharmaceutical;
KW mutant.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200022131-A2.
XX
PD 20-APR-2000.
XX
PF 13-OCT-1999; 99WO-US24065.
XX
XX 13-OCT-1999; 99WO-US24065.
XX
PR 13-OCT-1998; 98US-0170496.
PR 12-NOV-1998; 98US-0108029.
PR 20-NOV-1998; 98US-0109213.
PR 27-NOV-1998; 98US-0110060.
PR 16-FEB-1999; 99US-0120416.
PR 26-FEB-1999; 99US-0121852.
PR 12-MAR-1999; 99US-0123944.
PR 12-MAR-1999; 99US-0123945.
PR 12-MAR-1999; 99US-0123946.
PR 12-MAR-1999; 99US-0123948.
PR 12-MAR-1999; 99US-0123949.
PR 12-MAR-1999; 99US-0123951.
PR 28-MAY-1999; 99US-0136436.
PR 28-MAY-1999; 99US-0136437.
PR 28-MAY-1999; 99US-0136439.
PR 28-MAY-1999; 99US-0137127.

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PR 28-MAY-1999; 99US-0137131.
PR 28-MAY-1999; 99US-0137567.
PR 30-JUN-1999; 99US-0141448.
PR 27-AUG-1999; 99US-0151114.
PR 03-SEP-1999; 99US-0152524.
PR 29-SEP-1999; 99US-0156633.
PR 29-SEP-1999; 99US-0156555.
PR 29-SEP-1999; 99US-0156634.
XX
PA (AREN-) ARENA PHARM INC.
XX
XX Behan DP, Lehmann-Brusma K, Chalmers DT, Chen R, Dang HT;
PI Gore M, Liaw CW, Lin I, Lowitz K, White C;
XX WPI: 2000-317986/27.
DR N-PSDB; AAA46090.
XX
PT Non-endogenous, human G protein-coupled receptors for screening
PT receptor, inverse or partial agonists useful as therapeutic agents
XX
PS Example 2; Page 150-151; 187pp; English.
XX
CC The present invention describes transmembrane receptors, preferably
CC human G protein coupled receptors (GPCR), for which the endogenous
CC ligand is unknown (orphan GPCR receptors). More specifically the present
CC invention relates to non-endogenous, constitutively activated versions
CC of a human GPCR. These non-endogenous human GPCRs can be useful for
CC the direct identification of candidate compounds as receptors agonists,
CC inverse agonists or partial agonists for use as pharmaceutical agents.
CC AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
CC the exemplification of the present invention.
XX
SQ Sequence 359 AA;
Query Match 100.0%; Score 10; DB 21; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EDGIRKRIQDD 10
DB 8 EDGIRKRIQDD 17
XX
RESULT 7
AAO20951
ID AAO20951 standard; Protein; 359 AA.
XX
AC AAO20951;
XX
DT 11-JUL-2002 (first entry)
XX
DE Protein of the angiotensin II type 1 (AT-1) receptor.
XX
KW Cardiovascular; vasotropic; angiotensin II; aortic valve disease;
KW angiotensin converting enzyme; aortic valve; aortic stenosis; ACE;
KW inhibiting agent; angiotensin II type 1 receptor antagonist;
KW aortic sclerosis; AT-1.
XX
OS Homo sapiens.
XX
PN WO200228421-A1.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US31605.
XX
PR 06-OCT-2000; 2000US-238367P.
XX
PA (UNIW ) UNIV WASHINGTON.
XX
PI O'Brien KD, Otto CM, Probstfield JL;
XX WPI: 2002-372197/40.

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DR N-PSDB; AAK9740.
XX Decreasing the amount and/or biological activity of angiotensin II in
PT an aortic valve comprises administering angiotensin II inhibiting agent
PT consisting of antagonists of angiotensin converting enzyme and the
PT angiotensin II type I receptor
PS Disclosure; Page 36-37; 40pp; English.
XX
XX The invention relates to a method for decreasing the amount and/or
CC biological activity of angiotensin II in an aortic valve in an animal.
CC This method comprises administering an angiotensin II inhibiting agent
CC consisting of angiotensin converting enzyme (ACE) antagonists and
CC angiotensin II type I receptor antagonists. The method is also useful to
CC prevent progression and/or complications of aortic valve disease, such as
CC aortic stenosis or aortic sclerosis. This sequence represents the protein
CC of the angiotensin II type I (AT-1) receptor of the invention.
XX
SQ Sequence 359 AA;
Query Match 100.0%; Score 10; DB 23; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EDGKRIQDD 10
DB 8 EDGKRIQDD 17
IIIIIIIIII
RESULT 8
AAU78654
ID AAU78654 standard; Protein; 359 AA.
XX
AC AAU78654;
XX
XX 18-JUN-2002 (first entry)
DT
XX Human Angiotensin receptor 1, AGTRL.
DE
XX Human; angiotensin; receptor; AGTRL; hypotensive; hypertension;
KW chromosome 3q21-q25; haplotype; genotype; drug screening.
XX
XX Homo sapiens.
OS
XX EPI184456-A2.
PN
XX 06-MAR-2002.
PD
XX 12-JUN-2001; 2001EP-0114230.
PF
XX 28-AUG-2000; 2000US-228542P.
PR 30-MAY-2001; 2001US-0867915.
XX
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX Anastasio AE, Koshy B, Finkel K, Lee HH;
PI
XX MPI: 2002-282840/33.
DR N-PSDB; ABK47350, ABK47351.
DR
XX Novel genetic variants of Angiotensin Receptor 1 isogenes, useful for
PT improving efficiency and reliability in drug development for treating
PT diseases associated with AGTRL activity, e.g. hypertension
XX
XX Claim 30; Fig 3; 44pp; English.
PS
XX The invention relates to an isolated polynucleotide comprising a first
CC nucleotide sequence which comprises a angiotensin receptor 1 (AGTRL)
CC isogene selected from isogenes 1-8 and 10 given in the specification.
CC Also included are methods of haplotyping/genotyping the AGTRL gene
CC of an individual, predicting a haplotype pair of an individual,
CC identifying an association between a trait and at least one haplotype or
CC haplotype pair of AGTRL gene, oligonucleotides and primers for

CC detecting polymorphisms in the AGTRL gene, a recombinant non-human
CC organism transformed or transfected with an AGTRL gene, where the
CC organism expresses a AGTRL protein encoded by the AGTRL gene or the
CC polymorphic variant sequence, the polymorphic variant proteins of AGTRL,
CC an anti-AGTRL protein monoclonal antibody, a computer system for
CC storing and analyzing polymorphism data for the AGTRL gene and
CC a genome anthology for AGTRL gene. The polypeptide is useful in screening
CC for drugs targeting AGTRL that are useful for treating hypertension. The
CC methods are useful for improving the efficiency and reliability of
CC several steps in the discovery and development of drugs for treating
CC diseases associated with AGTRL activity. The methods are also useful for
CC screening compounds targeting AGTRL. The antibody is useful in
CC diagnostic, prognostic and therapeutic methods. The AGTRL gene is useful
CC in studying the expression and function of AGTRL, and in expressing AGTRL
CC protein for use in screening for candidate drugs to treat diseases
CC related to AGTRL activity. The AGTRL gene is also useful in studying the
CC effect of the variation on the biological activity of AGTRL as well as on
CC the binding affinity of candidate drugs targeting AGTRL for the treatment
CC of hypertension. The recombinant organism is useful for studying the
CC expression of AGTRL isogenes in vivo, for in vivo screening and testing
CC of drugs targeted against AGTRL protein, and for testing the efficacy of
CC therapeutic agents and compounds for treating hypertension in a
CC biological system. The gene for AGTRL is located on chromosome
CC 3q21-q25. The present sequence is the AGTRL protein sequence.
XX
SQ Sequence 359 AA;
Query Match 100.0%; Score 10; DB 23; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EDGKRIQDD 10
DB 8 EDGKRIQDD 17
IIIIIIIIII
RESULT 9
AAU78655
ID AAU78655 standard; Protein; 359 AA.
XX
AC AAU78655;
XX
XX 18-JUN-2002 (first entry)
DT
XX Human Angiotensin receptor 1, AGTRL, variant #1.
DE
XX Human; angiotensin; receptor; AGTRL; hypotensive; hypertension;
KW chromosome 3q21-q25; haplotype; genotype; drug screening.
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Misc-difference 204 /note="Wild-type Phe substituted by Ser"
FT
XX
XX EPI184456-A2.
PN
XX 06-MAR-2002.
PD
XX 12-JUN-2001; 2001EP-0114230.
PF
XX 28-AUG-2000; 2000US-228542P.
PR 30-MAY-2001; 2001US-0867915.
XX
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX Anastasio AE, Koshy B, Finkel K, Lee HH;
PI
XX MPI: 2002-282840/33.
DR
XX Novel genetic variants of Angiotensin Receptor 1 isogenes, useful for
PT improving efficiency and reliability in drug development for treating
PT diseases associated with AGTRL activity, e.g. hypertension
XX

XX Claim 30; Page -: 44pp; English.
PS The invention relates to an isolated polynucleotide comprising a first
XX nucleotide sequence which comprises a angiotensin receptor 1 (AGTRL)
CC isogene selected from isogenes 1-8 and 10 given in the specification.
CC Also included are methods of haplotyping/genotyping the AGTRL gene
XX of an individual, predicting a haplotype pair of an individual,
CC identifying an association between a trait and at least one haplotype or
CC haplotype pair of AGTRL gene, oligonucleotides and primers for
CC detecting polymorphisms in the AGTRL gene, a recombinant non-human
CC organism transformed or transfected with an AGTRL gene, where the
CC organism expresses a AGTRL protein encoded by the AGTRL gene or the
CC polymorphic variant sequence, the polymorphic variant proteins of AGTRL,
CC an anti-AGTRL protein monoclonal antibody, a computer system for
CC storing and analyzing polymorphism data for the AGTRL gene and
CC a genome anthology for AGTRL gene. The polypeptide is useful in screening
CC for drugs targeting AGTRL that are useful for treating hypertension. The
CC methods are useful for improving the efficiency and reliability of
CC several steps in the discovery and development of drugs for treating
CC diseases associated with AGTRL activity. The methods are also useful for
CC screening compounds targeting AGTRL. The antibody is useful in
CC diagnostic, prognostic and therapeutic methods. The AGTRL gene is useful
CC in studying the expression and function of AGTRL, and in expressing AGTRL
CC protein for use in screening for candidate drugs to treat diseases
CC related to AGTRL activity. The AGTRL gene is also useful in studying the
CC effect of the variation on the biological activity of AGTRL as well as on
CC the binding affinity of candidate drugs targeting AGTRL for the treatment
CC of hypertension. The recombinant organism is useful for studying the
CC expression of AGTRL isogenes in vivo, for in vivo screening and testing
CC of drugs targeted against AGTRL protein, and for testing the efficacy of
CC therapeutic agents and compounds for treating hypertension in a
CC biological system. The gene for AGTRL is located on chromosome
CC 3q21-q25. The present sequence is AGTRL variant protein sequence.
CC Note: The present sequence is not shown in the specification but
CC was created by the indexer using the AGTRL sequence appearing as
CC AAU78654 and the information in figure 3.
XX
XX SQ Sequence 359 AA;
Query Match 100.0%; Score 10; DB 23; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EDGKRIQDD 10
|||
Db 8 EDGKRIQDD 17
RESULT 10
AAU78656
ID AAU78656 standard; Protein: 359 AA.
XX
XX AC AAU78656;
XX
XX DT 18-JUN-2002 (first entry)
XX
XX DE Human Angiotensin receptor 1, AGTRL, variant #2.
XX
XX KM Human: angiotensin; receptor: AGTRL; hypotensive: hypertension;
XX chromosome 3q21-q25; haplotype; genotype; drug screening.
XX
XX OS Homo sapiens.
XX
XX FT Key Location/Qualifiers
XX Misc-difference 336
XX /note= "Wild-type Thr substituted by Met"
XX
XX PN EPI184456-A2.
XX
XX PD 06-MAR-2002.
XX
XX PF 12-JUN-2001; 2001EP-0114230.

XX 28-AUG-2000; 2000US-228542P.
PR 30-MAY-2001; 2001US-0867915.
XX
XX (GENA-) GENA1SSANCE PHARM INC.
XX
XX Anastasio AE, Koshy B, Finkel K, Lee HH;
XX WPI; 2002-282840/33.
XX
XX PT Novel genetic variants of Angiotensin Receptor 1 isogenes, useful for
XX improving efficiency and reliability in drug development for treating
XX diseases associated with AGTRL activity, e.g. hypertension
XX
XX Claim 30; Page -: 44pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising a first
XX nucleotide sequence which comprises a angiotensin receptor 1 (AGTRL)
XX isogene selected from isogenes 1-8 and 10 given in the specification.
XX Also included are methods of haplotyping/genotyping the AGTRL gene
XX of an individual, predicting a haplotype pair of an individual,
XX identifying an association between a trait and at least one haplotype or
XX haplotype pair of AGTRL gene, oligonucleotides and primers for
XX detecting polymorphisms in the AGTRL gene, a recombinant non-human
XX organism transformed or transfected with an AGTRL gene, where the
XX organism expresses a AGTRL protein encoded by the AGTRL gene or the
XX polymorphic variant sequence, the polymorphic variant proteins of AGTRL,
XX an anti-AGTRL protein monoclonal antibody, a computer system for
XX storing and analyzing polymorphism data for the AGTRL gene and
XX a genome anthology for AGTRL gene. The polypeptide is useful in screening
XX for drugs targeting AGTRL that are useful for treating hypertension. The
XX methods are useful for improving the efficiency and reliability of
XX several steps in the discovery and development of drugs for treating
XX diseases associated with AGTRL activity. The methods are also useful for
XX screening compounds targeting AGTRL. The antibody is useful in
XX diagnostic, prognostic and therapeutic methods. The AGTRL gene is useful
XX in studying the expression and function of AGTRL, and in expressing AGTRL
XX protein for use in screening for candidate drugs to treat diseases
XX related to AGTRL activity. The AGTRL gene is also useful in studying the
XX effect of the variation on the biological activity of AGTRL as well as on
XX the binding affinity of candidate drugs targeting AGTRL for the treatment
XX of hypertension. The recombinant organism is useful for studying the
XX expression of AGTRL isogenes in vivo, for in vivo screening and testing
XX of drugs targeted against AGTRL protein, and for testing the efficacy of
XX therapeutic agents and compounds for treating hypertension in a
XX biological system. The gene for AGTRL is located on chromosome
XX 3q21-q25. The present sequence is AGTRL variant protein sequence.
XX Note: The present sequence is not shown in the specification but
XX was created by the indexer using the AGTRL sequence appearing as
XX AAU78654 and the information in figure 3.
XX
XX SQ Sequence 359 AA;
Query Match 100.0%; Score 10; DB 23; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EDGKRIQDD 10
|||
Db 8 EDGKRIQDD 17
RESULT 11
AAB02851
ID AAB02851 standard; Protein: 360 AA.
XX
XX AC AAB02851;
XX
XX DT 22-AUG-2000 (first entry)
XX
XX DE Human G protein coupled receptor hAT1 mutant protein SEQ ID NO:106.
XX
XX KM Human; G protein coupled receptor; GPCR; transmembrane receptor;

KW Identification; agonist; screening; therapeutic; pharmaceutical;
 mutant.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200022131-A2.
 XX
 PD 20-APR-2000.
 XX
 PF 13-OCT-1999; 99WO-US24065.
 XX
 PR 13-OCT-1998; 98US-0170496.
 PR 12-NOV-1998; 98US-0108029.
 PR 20-NOV-1998; 98US-0109213.
 PR 27-NOV-1998; 98US-0110060.
 PR 16-FEB-1999; 99US-0120416.
 PR 26-FEB-1999; 99US-0121852.
 PR 12-MAR-1999; 99US-0123944.
 PR 12-MAR-1999; 99US-0123945.
 PR 12-MAR-1999; 99US-0123946.
 PR 12-MAR-1999; 99US-0123948.
 PR 12-MAR-1999; 99US-0123949.
 PR 12-MAR-1999; 99US-0123951.
 PR 28-MAY-1999; 99US-0136436.
 PR 28-MAY-1999; 99US-0136437.
 PR 28-MAY-1999; 99US-0136439.
 PR 28-MAY-1999; 99US-0137127.
 PR 28-MAY-1999; 99US-0137131.
 PR 28-MAY-1999; 99US-0137567.
 PR 30-JUN-1999; 99US-0141448.
 PR 27-AUG-1999; 99US-0151114.
 PR 03-SEP-1999; 99US-0152524.
 PR 29-SEP-1999; 99US-0156533.
 PR 29-SEP-1999; 99US-0156555.
 PR 29-SEP-1999; 99US-0156634.
 XX
 PA (AREN-) ARENA PHARM INC.
 XX
 PI Behan DP, Lehmann-Brulsma K, Chalmers DT, Chen R, Dang HT;
 PI Gore M, Flaw CW, Lin I, Lowitz K, White C;
 XX
 DR WPI: 2000-317986/27.
 DR N-PSDB: AAA46095.
 XX
 PT Non-endogenous, human G protein-coupled receptors for screening
 PT receptor, inverse or partial agonists useful as therapeutic agents -
 XX
 PS Example 2; Page 153-155; 187pp; English.
 XX
 CC The present invention describes transmembrane receptors, preferably
 CC human G protein coupled receptors (GPCR), for which the endogenous
 CC ligand is unknown (orphan GPCR receptors). More specifically the present
 CC invention relates to non-endogenous, constitutively activated versions
 CC of a human GPCR. These non-endogenous human GPCRs can be useful for
 CC the direct identification of candidate compounds as receptors agonists,
 CC inverse agonists or partial agonists for use as pharmaceutical agents.
 CC AAA6017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
 CC the exemplification of the present invention.
 XX
 SQ Sequence 360 AA:

Query Match 100.0%; Score 10; DB 21; Length 360;
 Best Local Similarity 100.0%; Pred. No. 0.00086;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGIRIOPD 10
 |||||||||
 DB 8 EDGIRIOPD 17

RESULT 12
 AAR67111

ID AAR67111 standard; peptide; 13 AA.
 XX
 AC AAR67111;
 XX
 DT 30-JUN-1995 (first entry)
 XX
 DE Anti-contraction peptide (ACFP-ATIRA) contg. proline brackets.
 XX
 KW anti-contraction peptide; angiotensin II receptor type I;
 KW mimic; interaction site; constrained conformation; premature labour.
 XX
 OS Synthetic.
 XX
 PN WO9425482-A.
 XX
 PD 10-NOV-1994.
 XX
 PF 21-APR-1994; 94WO-US04294.
 XX
 PR 23-APR-1993; 93US-0051741.
 PR 29-OCT-1993; 93US-0143364.
 XX
 PA (EVAN/) EVANS H J.
 PA (KINI/) KINI R M.
 XX
 PI Evans HJ, Kini RM;
 XX
 DR WPI: 1994-358186/44.
 XX
 PT Peptide homologue or analogue with constrained conformation - has
 PT proline residues flanking the interaction site to impart greater,
 PT or more stable, biological activity
 XX
 PS Example 3; Page 38; 57pp; English.
 XX
 CC AAR67111-13 are anti-contraction peptides derived from naturally
 CC occurring polypeptides that contain proline or proline/cysteine brackets.
 CC These peptides are shortened to form fragments that contain one or more
 CC interaction sites of interest. AAR67111-113 are deriv. from angiotensin
 CC II receptor (type I). The dose is 1-200 micromoles. The peptides
 CC interact with angiotensin II and inhibits its ability to induce
 CC contraction. The data collected demonstrates that interaction sites
 CC possess activity when present in a polypeptide that differs from the
 CC native form. Inclusion of conformation-constraining moieties can have
 CC desirable effects on an interaction site. (Also see AAR67011-110 and
 CC AAR67114-52 for analogues of other biologically active peptides contg. an
 CC interaction site flanked by conformation constraining gps., eg. RGD
 CC peptides.)
 XX
 SQ Sequence 13 AA:

Query Match 70.0%; Score 7; DB 15; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 IKRIOPD 10
 |||||||
 DB 3 IKRIOPD 9

RESULT 13
 AAG11661
 ID AAG11661 standard; Protein; 62 AA.
 XX
 AC AAG11661;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 10462.
 XX
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

XX Arabidopsis thaliana.
OS
XX EPI033405-A2.
PN
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
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PR 17-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
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PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.

PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
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PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
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PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
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PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
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PR 17-AUG-1999; 99US-0149175.
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PR 20-AUG-1999; 99US-0149929.
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PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151308.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.


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PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
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PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
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PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
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PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 60.0%; Score 6; DB 21; Length 62;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 KRIQDD 10
DB 33 KRIQDD 38

RESULT 14
AAM26782
ID AAM26782 standard; Protein: 440 AA.
XX
AC AAM26782;
XX
XX 08-JUN-1998 (first entry)
DE Mouse Friend virus susceptibility 1 gene (Fv1n allele) protein.
XX Friend virus susceptibility gene; Fv1; Fv1n; mouse; retrovirus;
KM Infection; antiviral; virucide.
XX
XX Mus musculus strain AKR/J.
XX
XX MO9743410-A1.
XX
XX 20-NOV-1997.
XX
XX 14-MAY-1997; 97WO-GB01311.
```

```
XX
PR 14-MAY-1996; 96GB-0009995.
XX
XX (MEDI-) MEDICAL RES COUNCIL.
XX
XX Le Tissier PR; Stoye JP;
XX
XX WPI; 1998-008879/01.
XX
XX N-PSDB; AAT99573.
XX
XX Murine Friend virus susceptibility 1 gene polypeptide - which
XX inhibits retroviral integration into newly infected cells, useful in
XX antiviral agent development
XX
XX Claim 1; Page 41-44; 55pp; English.
XX
XX This polypeptide is the encoded product of the Fv1n allele (see
XX AAT99573) of the Friend virus susceptibility 1 (Fv1) gene located
XX on mouse chromosome 4. It differs in the C-terminal region from
XX the Fv1 protein (see AAM26781) encoded by the Fv1b allele (see
XX AAT99572) isolated from mouse strain C57BL/6 and additionally differs
XX at amino acids 358 and 399. Fv1 transcripts can not be detected
XX by Northern blotting, suggesting very low levels of in vivo
XX expression. Claimed host cells can be used for the recombinant
XX production of Fv1 polypeptide. The polypeptide inhibits retroviral
XX integration into newly infected cells. Fragments of the
XX polypeptide can be used as antiviral agents. Modulators of the
XX polypeptide, or modified forms of the polypeptide, may be useful
XX for inhibiting retroviral replication.
XX
XX Sequence 440 AA;
SQ
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Query Match 60.0%; Score 6; DB 19; Length 440;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGIRK 6
DB 354 EDGIRK 359

RESULT 15
ABB65401
ID ABB65401 standard; Protein: 442 AA.
XX
XX ABB65401;
XX
XX 26-MAR-2002 (first entry)
DE Drosophila melanogaster polypeptide SEQ ID NO 22995.
XX
XX Drosophila melanogaster polypeptide seq ID NO 22995.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
XX
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX
XX N-PSDB; ABL09504.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
```

PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Disclosure; SEQ ID NO 22995; 21np + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 442 AA:

Query Match 60.0%; Score 6; DB 22; Length 442;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative, 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPGIKR 6
|||
Db 272 EDGIKR 277

Search completed: November 12, 2002, 16:19:11
Job time : 36 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:18:18 ; Search time 16 Seconds
(without alignments)
60.084 Million cell updates/sec

Title: US-09-540-816-1

Perfect score: 10

Sequence: 1 EDGIRIQQDD 10

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR_73:*

1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	100.0	359	2 JCI104	angiotensin II rec
2	10	100.0	359	2 S44425	angiotensin II rec
3	10	100.0	359	2 JCI194	angiotensin II rec
4	10	100.0	359	2 A48857	angiotensin II rec
5	10	100.0	359	2 A42656	angiotensin II rec
6	10	100.0	359	2 J01516	angiotensin II rec
7	10	100.0	359	2 S15403	angiotensin II rec
8	10	100.0	359	2 I38418	angiotensin II rec
9	10	100.0	359	2 JH0621	angiotensin II rec
10	10	100.0	359	2 JC2134	angiotensin II rec
11	6	60.0	126	2 E84420	probable ubiquinol
12	6	60.0	126	2 S29303	hypothetical prote
13	6	60.0	228	2 S34646	fibritarlin-like p
14	6	60.0	254	2 A64437	hypothetical prote
15	6	60.0	348	2 T07660	probable serine/th
16	6	60.0	426	2 D83890	sugar transport sy
17	6	60.0	447	2 E83015	heat shock protein
18	6	60.0	472	2 T19375	hypothetical prote
19	6	60.0	504	2 T07415	probable serine/th
20	6	60.0	509	1 S04346	steroid 17alpha-mo
21	6	60.0	586	1 VGVNBF	nonstructural glyco
22	6	60.0	611	2 S19434	hypothetical prote
23	6	60.0	785	2 S46672	hypothetical prote
24	6	60.0	1166	2 C84532	copla-like retroel
25	5	50.0	32	2 E82089	hypothetical prote
26	5	50.0	79	1 LNRG1	pulmonary surfacta
27	5	50.0	81	2 C83792	hypothetical prote
28	5	50.0	89	2 D96034	conserved hypothet
29	5	50.0	98	2 D97014	hypothetical prote

30	5	50.0	104	2 T19868	hypothetical prote
31	5	50.0	110	2 S17709	kdsf protein - Brw
32	5	50.0	116	2 S71438	probable glutamate
33	5	50.0	116	2 A87135	hypothetical prote
34	5	50.0	118	2 T37269	hypothetical prote
35	5	50.0	119	2 A90219	15U ribosomal prot
36	5	50.0	121	2 S50000	ribosomal protein
37	5	50.0	126	2 B70575	probable hsp90 prot
38	5	50.0	132	2 B87221	heat shock regulat
39	5	50.0	137	2 S37723	hypothetical 14.9k
40	5	50.0	145	2 B28151	globin chain b, ex
41	5	50.0	145	2 A95015	hypothetical prote
42	5	50.0	145	2 B97888	ribosomal-protein-
43	5	50.0	149	2 E83822	transposase relate
44	5	50.0	151	2 S70209	regulatory protein
45	5	50.0	153	2 D89940	hypothetical prote

ALIGNMENTS

RESULT 1
JCI104
angiotensin II receptor type 1 - human
N:Alternate names: angiotensin II receptor 1A
C:Species: Homo sapiens (man)
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jul-2000
C:Accession: JCI104; J01402; JH0574; JH0267; A44014; S18983
R:Maury, C.A.; Hwang, O.; Egloff, A.M.; Wu, L.H.; Chung, F.Z.
R:Biochem. Biophys. Res. Commun. 186, 277-284, 1992
A>Title: Cloning, expression, and characterization of a gene encoding the human angio
A:Reference number: JCI104; MUID:92337608; PMID:1376723
A:Accession: JCI104
A:Molecule type: DNA
A:Residues: 1-359 <MAU>
R:Furuta, H.; Guo, D.F.; Inagami, T.
R:Biochem. Biophys. Res. Commun. 183, 8-13, 1992
A>Title: Molecular cloning and sequencing of the gene encoding human angiotensin II t
A:Reference number: J01402; MUID:92181475; PMID:1543512
A:Accession: J01402
A:Molecule type: DNA
A:Residues: 1-359 <FUR>
A:Cross-references: EMBL:Z11162; NID:928709; PID:928710
A:Experimental source: Lymphocyte
R:Bergsm, D.J.; Ellis, C.; Kumar, C.; Nuthulaganti, P.; Kersten, H.; Elshourbagy, N.
R:Biochem. Biophys. Res. Commun. 183, 989-995, 1992
A>Title: Cloning and characterization of a human angiotensin II type 1 receptor.
A:Reference number: JH0574; MUID:92231907; PMID:1567413
A:Accession: JH0574
A:Molecule type: mRNA
A:Residues: 1-359 <BER>
A:Cross-references: GB:M87290; NID:9178682; PID:NAA35535.1; PID:9178683
A:Experimental source: Liver
R:Takayanagi, R.; Ohnaka, K.; Sakai, Y.; Nakao, R.; Yanase, T.; Hagi, M.; Inagami, T.
R:Biochem. Biophys. Res. Commun. 183, 910-916, 1992
A>Title: Molecular cloning, sequence analysis and expression of a cDNA encoding human
A:Reference number: JH0267; MUID:92198490; PMID:1550596
A:Accession: JH0267
A:Molecule type: mRNA
A:Residues: 1-359 <TAK>
A:Experimental source: Liver
R:Currow, K.M.; Pascoe, L.; White, P.C.
R:Mol. Endocrinol. 6, 1113-1118, 1992
A>Title: Genetic analysis of the human type-1 angiotensin II receptor.
A:Reference number: A44014; MUID:92375105; PMID:1508224
A:Accession: A44014
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <CUR>
A:Cross-references: GB:M93394; NID:9178680; PID:9178681
A:Note: sequence extracted from NCBI backbone (NCBIN:111831, NCBIP:111833)
C:Genetics:
A:Gene: GDB:AGTR1

A:Cross-references: GDB:132359; OMIM:106165
A:Map position: 3q21-3q25
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; transmembrane pr
F:30-53/Domain: transmembrane #status predicted <TM1>
F:65-90/Domain: transmembrane #status predicted <TM2>
F:103-124/Domain: transmembrane #status predicted <TM3>
F:145-167/Domain: transmembrane #status predicted <TM4>
F:194-216/Domain: transmembrane #status predicted <TM5>
F:241-264/Domain: transmembrane #status predicted <TM6>
F:281-305/Domain: transmembrane #status predicted <TM7>
F:4,176,188/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 100.0%; Score 10; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.00078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGIRKRIQDD 10
|||||
DB 8 EDGIRKRIQDD 17

RESULT 2
S44425
angiotensin II receptor type 1 - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C:Accession: S44425
R:Burns, L.; Clark, K.L.; Bradley, J.; Robertson, M.J.; Clark, A.J.L.
FEBS Lett. 343, 146-150, 1994
A>Title: Molecular cloning of the canine angiotensin II receptor. An AT1-like receptor
A:Reference number: S44425; MUID:94222188; PMID:8168620
A:Accession: S44425
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-359 <BUN>
A:Cross-references: PIDN:AAB30674.1; PID:9546566
A:Experimental source: liver
C:Superfamily: vertebrate rhodopsin

Query Match 100.0%; Score 10; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.00078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGIRKRIQDD 10
|||||
DB 8 EDGIRKRIQDD 17

RESULT 3
JC1194
angiotensin II receptor 1B - mouse
C:Species: Mus musculus (house mouse)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 05-Nov-1999
C:Accession: JC1194; JH0622
R:Yoshida, H.; Kakuchi, J.; Guo, D.F.; Furuta, H.; Iwai, N.; van der Meer-de Jong, R.; I
Biochem. Biophys. Res. Commun. 186, 1042-1049, 1992
A>Title: Analysis of the evolution of angiotensin II type 1 receptor gene in mammals (mc
A:Reference number: JC1193; MUID:92259981; PMID:1497638
A:Accession: JC1194
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-359 <YOS>
R:Sasamura, H.; Hein, L.; Krieger, J.E.; Pratt, R.E.; Koblika, B.K.; Dzau, V.J.
Biochem. Biophys. Res. Commun. 185, 253-259, 1992
A>Title: Cloning, characterization, and expression of two angiotensin receptor (AT-1) is
A:Reference number: JH0622; MUID:92287102; PMID:1599461
A:Accession: JH0622
A:Molecule type: DNA
A:Residues: 1-6, 'I', '8-165, 'H', '167-172, 'E', '174-204, 'V', '206-231, 'T', '233-238, 'F', '240-359 <S
A:Cross-references: GB:S37491; NID:92449947; PIDN:AAB22270.1; PID:92449948
A:Experimental source: Balb/c
C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p
F:30-53/Domain: transmembrane #status predicted <TM1>
F:65-90/Domain: transmembrane #status predicted <TM2>
F:103-123/Domain: transmembrane #status predicted <TM3>
F:147-166/Domain: transmembrane #status predicted <TM4>
F:195-218/Domain: transmembrane #status predicted <TM5>
F:240-263/Domain: transmembrane #status predicted <TM6>
F:278-300/Domain: transmembrane #status predicted <TM7>
F:4,176,188/Binding site: carbohydrate (asn) (covalent) #status predicted
F:141/Binding site: phosphate (Thr) (covalent) #status predicted
F:331,338,348/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 100.0%; Score 10; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.00078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGIRKRIQDD 10
|||||
DB 8 EDGIRKRIQDD 17

RESULT 4
A48857
angiotensin II receptor type 1 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C:Accession: A48857
R:Burns, K.D.; Inagami, T.; Harris, R.C.
Am. J. Physiol. 264, F645-F654, 1993
A>Title: Cloning of a rabbit kidney cortex AT1 angiotensin II receptor that is presen
A:Reference number: A48857; MUID:93236091; PMID:7916579
A:Accession: A48857
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-359 <BUN>
A:Cross-references: GB:S59041; NID:9299614; PIDN:AAB26239.1; PID:9299615
A:Experimental source: proximal tubule cells
A:Note: sequence extracted from NCBI backbone (NCBIN:129600, NCBI:P:129601)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 100.0%; Score 10; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.00078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGIRKRIQDD 10
|||||
DB 8 EDGIRKRIQDD 17

RESULT 5
A42656
angiotensin II receptor type 1B (AT3) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C:Accession: A42656; S20423
R:Sandberg, K.; Ji, H.; Clark, A.J.; Shapira, H.; Catt, K.J.
J. Biol. Chem. 267, 9455-9458, 1992
A>Title: Cloning and expression of a novel angiotensin II receptor subtype.
A:Reference number: A42656; MUID:92250585; PMID:1374402
A:Accession: A42656
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <SAN>
A:Cross-references: GB:M90065; NID:9202801; PIDN:AAA40704.1; PID:9202802
A:Experimental source: adrenal cortex
A:Note: sequence extracted from NCBI backbone (NCBIN:100262, NCBI:P:100268)
R:Iwai, N.; Inagami, T.
FEBS Lett. 298, 257-260, 1992
A>Title: Identification of two subtypes in the rat type I angiotensin II receptor.
A:Reference number: S20423; MUID:92183879; PMID:1544458
A:Accession: S20423

A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-359 <IWM>
 A:Cross-references: GB:X64052; NID:g57521; PIDN:CAA5410.1; PID:g57522
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 100.0%; Score 10; DB 2; Length 359;
 Best Local Similarity 100.0%; Pred. No. 0.00078;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGIRRIODD 10
 |||||
 DB 8 EDGIRRIODD 17

RESULT 6

J01516
 angiotensin II receptor type 1B - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999
 C:Accession: J01516; J0578; PH0850
 R:Elton, T.S.; Stephan, C.C.; Taylor, G.R.; Kimball, M.G.; Martin, M.M.; Durand, J.N.; C
 Biochem. Biophys. Res. Commun. 184, 1067-1073, 1992
 A:Title: Isolation of two distinct type 1 angiotensin II receptor genes.
 A:Reference number: J01516; MUID:92246922; PMID:1575725
 A:Accession: J01516
 A:Molecule type: DNA
 A:Residues: 1-359 <ELT>
 A:Note: The authors translated the codon AGC for residue 120 as Thr, GTC for residue 225
 R:Kakar, S.S.; Sellers, J.C.; Devor, D.C.; Musgrove, L.C.; Neill, J.D.
 Biochem. Biophys. Res. Commun. 183, 1090-1096, 1992
 A:Title: Angiotensin II type-1 receptor subtype cDNAs: differential tissue expression at
 A:Reference number: J00578; MUID:92231868; PMID:1567388
 A:Accession: J00578
 A:Molecule type: mRNA
 A:Residues: 1-74, 'L', '76-119, 'T', '121-224, 'A', '226-359 <RKR>
 A:Cross-references: GB:M87003; NID:g202920; PIDN:AAA40739.1; PID:g202921
 A:Experimental source: anterior pituitary
 R:Ye, M.Q.; Healy, D.P.
 Biochem. Biophys. Res. Commun. 185, 204-210, 1992
 A:Title: Characterization of an angiotensin type-1 receptor partial cDNA from rat kidney
 A:Reference number: PH0850; MUID:92287094; PMID:1599457
 A:Accession: PH0850
 A:Molecule type: mRNA
 A:Residues: 84-119, 'T', '121-224, 'A', '226-259 <YEM>
 A:Cross-references: GB:S37461; NID:g249938; PIDN:AB22267.1; PID:g249939
 A:Experimental source: kidney
 C:Genetics:
 A:Gene: AT1B
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot

F:27-53/Domain: transmembrane #status predicted <TMW1>
 F:65-90/Domain: transmembrane #status predicted <TMW2>
 F:103-135/Domain: transmembrane #status predicted <TMW3>
 F:145-166/Domain: transmembrane #status predicted <TMW4>
 F:194-216/Domain: transmembrane #status predicted <TMW5>
 F:240-264/Domain: transmembrane #status predicted <TMW6>
 F:278-304/Domain: transmembrane #status predicted <TMW7>
 F:4,176,188,344/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:232,333/Binding site: phosphate (Thr) (covalent) #status predicted
 F:331,338,348/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 100.0%; Score 10; DB 2; Length 359;
 Best Local Similarity 100.0%; Pred. No. 0.00078;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGIRRIODD 10
 |||||
 DB 8 EDGIRRIODD 17

RESULT 7

S15403
 angiotensin II receptor type 1 - bovine
 C:Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
 C:Accession: S15403
 R:Sasaki, K.; Yamano, Y.; Bardhan, S.; Iwai, N.; Murray, J.J.; Hasegawa, M.; Matsuda,
 Nature 351, 230-233, 1991
 A:Title: Cloning and expression of a complementary DNA encoding a bovine adrenal angt
 A:Reference number: S15403; MUID:91251900; PMID:2041569
 A:Accession: S15403
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-359 <SAS>
 A:Cross-references: GB:X62294; NID:g43; PIDN:CAA44182.1; PID:g44
 C:Superfamily: vertebrate rhodopsin

Query Match 100.0%; Score 10; DB 2; Length 359;
 Best Local Similarity 100.0%; Pred. No. 0.00078;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGIRRIODD 10
 |||||
 DB 8 EDGIRRIODD 17

RESULT 8

I39418
 angiotensin II receptor type 1b - human
 C:Species: Homo sapiens (man)
 C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 24-Nov-1999
 C:Accession: I39418
 R:Kuroda, S.
 Biochem. Biophys. Res. Commun. 199, 467-474, 1994
 A:Title: Novel subtype of human angiotensin II type 1 receptor: cDNA cloning and expr
 A:Reference number: I39418; MUID:94183213; PMID:8135787
 A:Accession: I39418
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-359 <RES>
 A:Cross-references: GB:D13814; NID:g471120; PIDN:BA02968.1; PID:g471121
 C:Superfamily: vertebrate rhodopsin

Query Match 100.0%; Score 10; DB 2; Length 359;
 Best Local Similarity 100.0%; Pred. No. 0.00078;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGIRRIODD 10
 |||||
 DB 8 EDGIRRIODD 17

RESULT 9

JH0621
 angiotensin II receptor 1A - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 24-Nov-1999
 C:Accession: JH0621; J01193
 R:Sasamura, H.; Hein, L.; Krieger, J.E.; Pratt, R.E.; Kobilka, B.K.; Dzau, V.J.
 Biochem. Biophys. Res. Commun. 185, 253-259, 1992
 A:Title: Cloning, characterization, and expression of two angiotensin receptor (AT-1)
 A:Reference number: JH0621; MUID:92287102; PMID:1599461
 A:Accession: JH0621
 A:Molecule type: DNA
 A:Residues: 1-359 <SAS>
 A:Cross-references: GB:S37484; NID:g249945; PIDN:AB22269.1; PID:g249946
 A:Experimental source: strain Balb/c
 R:Yoshida, H.; Kakuchi, J.; Guo, D.F.; Furuta, H.; Iwai, N.; van der Meer-de Jong, R.
 Biochem. Biophys. Res. Commun. 186, 1042-1049, 1992
 A:Title: Analysis of the evolution of angiotensin II type 1 receptor gene in mammals
 A:Reference number: J01193; MUID:92359981; PMID:1497638
 A:Accession: J01193
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA

Query Match 100.0%; Score 10; DB 2; Length 359;
 Best Local Similarity 100.0%; Pred. No. 0.00078;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

A:Residues: 1-6,'I',8-19,'IS',22-37,'W',39-133,'K',135-359 <YOS>
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
 F:37-57/Domain: transmembrane #status predicted <TM1>
 F:65-85/Domain: transmembrane #status predicted <TM2>
 F:103-123/Domain: transmembrane #status predicted <TM3>
 F:145-165/Domain: transmembrane #status predicted <TM4>
 F:201-220/Domain: transmembrane #status predicted <TM5>
 F:241-261/Domain: transmembrane #status predicted <TM6>
 F:286-306/Domain: transmembrane #status predicted <TM7>
 F:4,176,188/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:331,338/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 100.0%; Score 10; DB 2; Length 359;
 Best Local Similarity 100.0%; Pred. No. 0.00078;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGIRKIQDD 10
 Db 8 EDGIRKIQDD 17

RESULT 10
 JG2134
 angiotensin II receptor type 1A - rat
 N:Alternate names: AT1a receptor; AT3 receptor
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 24-Nov-1999
 C:Accession: JG2134; S15404; S20424; J01055
 R:Conchon, S.; Monnot, C.; Strleix, M.E.; Bihoreau, C.; Corvol, P.; Clausen, E.
 Biochem. Biophys. Res. Commun. 199, 1347-1354, 1994
 A:Title: Synthetic cDNA encoding the rat AT1a receptor: a useful tool for structure-func
 A:Reference number: JC2134; MUID:94197726; PMID:8147879
 A:Accession: JC2134
 A:Molecule type: mRNA
 A:Residues: 1-359 <CON>
 A:Note: the amino acid sequence of this protein is not given
 R:Murphy, T.J.; Alexander, R.W.; Griendling, K.K.; Runge, M.S.; Bernstein, K.E.
 Nature 351, 233-236, 1991
 A:Title: Isolation of a cDNA encoding the vascular type-1 angiotensin II receptor.
 A:Reference number: S15404; MUID:91251901; PMID:2041570
 A:Accession: S15404
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-359 <MUR>
 A:Cross-references: GS:X62295; NID:957773; PIDN:CAA44183.1; PID:957774
 R:Iwai, N.; Inagami, T.
 FEBS Lett. 298, 257-260, 1992
 A:Title: Identification of two subtypes in the rat type I angiotensin II receptor.
 A:Reference number: S20423; MUID:92183879; PMID:1544458
 A:Accession: S20424
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-359 <IMA>
 R:Iwai, N.; Yamano, Y.; Chaki, S.; Konishi, F.; Bardhan, S.; Tibbets, C.; Sasaki, K.; H
 Biochem. Biophys. Res. Commun. 177, 299-304, 1991
 A:Title: Rat angiotensin II receptor: cDNA sequence and regulation of the gene expressio
 A:Reference number: J01055; MUID:91254291; PMID:2043116
 A:Accession: J01055
 A:Molecule type: mRNA
 A:Residues: 1-60,'C',82-108,'T',110-359 <IW2>
 A:Cross-references: GB:M74054; NID:9202918; PIDN:AAA40738.1; PID:9202919
 A:Experimental source: kidney
 C:Comment: AT1 receptor consists of two closely related AT1 isoforms of angiotensin II r
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; GTP binding; receptor; transmembra
 F:27-86/Domain: transmembrane #status predicted <TM1>
 F:103-123/Domain: transmembrane #status predicted <TM2>
 F:147-167/Domain: transmembrane #status predicted <TM3>
 F:195-218/Domain: transmembrane #status predicted <TM4>
 F:240-263/Domain: transmembrane #status predicted <TM5>
 F:278-299/Domain: transmembrane #status predicted <TM6>
 F:4,176,188/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 10; DB 2; Length 359;
 Best Local Similarity 100.0%; Pred. No. 0.00078;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGIRKIQDD 10
 Db 8 EDGIRKIQDD 17

RESULT 11
 E84420
 Probable ubiquinol-cytochrome c reductase [Imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 17-May-2002
 C:Accession: E84420
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Beilto, M.I.; Town, C.D.; Fujii, C.Y
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon,
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617157
 A:Accession: E84420
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-62 <STO>
 A:Cross-references: GB:AE002093; NID:96598624; PIDN:AF18657.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: AC2901090
 A:Map position: 2
 C:Superfamily: ubiquinol-cytochrome-c reductase 11k protein; ubiquinol-cytochrome-c r

Query Match 60.0%; Score 6; DB 2; Length 62;
 Best Local Similarity 100.0%; Pred. No. 4.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KRIQDD 10
 Db 33 KRIQDD 38

RESULT 12
 S29303
 hypothetical protein 1 (phac1 5' region) - Pseudomonas aeruginosa (fragment)
 C:Species: Pseudomonas aeruginosa
 C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 08-Oct-1999
 C:Accession: S29303; S28375
 R:Timm, A.; Steinduechel, A.
 Eur. J. Biochem. 209, 15-30, 1992
 A:Title: Cloning and molecular analysis of the poly(3-hydroxyalkanoic acid) gene locu
 A:Reference number: S29303; MUID:93011120; PMID:1396693
 A:Accession: S29303
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-126 <TIM>
 A:Cross-references: EMBL:X66592; NID:945388; PIDN:CAA47149.1; PID:945389
 C:Superfamily: heat shock protein hslu; FSH/SEC18/CDc48-type ATP-binding domain homo

Query Match 60.0%; Score 6; DB 2; Length 126;
 Best Local Similarity 100.0%; Pred. No. 7.9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGIRK 6
 Db 49 EDGIRK 54

RESULT 13
 S34646
 fibrillarin-like protein - Methanococcus voltae
 N:Alternate names: pre-tRNA-processing protein
 C:Species: Methanococcus voltae
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999

C:Accession: S34646
R:Agna Amir, K.
Submitted to the EMBL Data Library, July 1993
A:Description: A fibrillarlin like protein occurs in archaea.
A:Reference number: S34645
A:Accession: S34646
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-228 <AGH>
A:Cross-references: EMBL:X73988; NID:G394799; PIDN:CAA52166.1; PID:G394800
C:Genetics:
A:Gene: rppA
C:Superfamily: human fibrillarlin

Query Match 60.0%; Score 6; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGIRRI 7
|||||
DB 18 DGIRRI 23

RESULT 14
A64437
hypothetical protein MJ1098 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: A64437
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Bordovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: A64437
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-254 <BUL>
A:Cross-references: GB:U67552; GB:L77117; NID:G1591737; PIDN:AAB99101.1; PID:G1591742; T
C:Genetics:
A:Map position: REV1039390-1038626
A:Start codon: TTG

Query Match 60.0%; Score 6; DB 2; Length 254;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGIRRI 7
|||||
DB 139 DGIRRI 144

RESULT 15
T07660
probable serine/threonine-specific protein kinase (EC 2.7.1.-) PKIN1 - potato (fragment)
N:Alternate names: SNF1-related protein kinase
C:Species: Solanum tuberosum (potato)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C:Accession: T07660
R:Man, A.L.; Purcell, P.C.; Hannappel, U.; Halford, N.G.
Plant Mol. Biol. 34, 31-43, 1997
A:Title: Potato SNF1-related protein kinase: molecular cloning, expression analysis and
A:Reference number: Z16075; MUID:97320459; PMID:9177310
A:Accession: T07660
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-348 <MAN>
A:Cross-references: EMBL:X95996; NID:G1216284; PIDN:CAA65243.1; PID:G1216285
A:Experimental source: cv. Désirée; developing tuber
C:Genetics:
A:Gene: PKIN1

C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threo
C:Superfamily: AMP-activated protein kinase; protein kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

Query Match 60.0%; Score 6; DB 2; Length 348;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 KRIQDD 10
|||||
DB 159 KRIQDD 164

Search completed: November 12, 2002, 16:20:31
Job time : 18 secs

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